



#3

SEQUENCE LISTING

<110> Haas, Rainald
Kleanthous, Harold
Tomb, Jean-Francois
Miller, Charles
Al-Garawi, Amal
Odenbreit, Stefan
Meyer, Thomas

<120> Helicobacter Polypeptides and
Corresponding Polynucleotide Molecules

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<140> US 09/988,067

<141> 2001-11-16

<150> US 08/831,309

<151> 1997-04-01

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caa gcc ttt atc att ccc tct cgc tct atg gtt ggc acg ctc tat gag 205
Gln Ala Phe Ile Ile Pro Ser Arg Ser Met Val Gly Thr Leu Tyr Glu
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Gly Asp Met Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile Pro
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Lys Ile Pro Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn Asn

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His Pro Phe Glu Ser Asp Thr Asp Lys Asn Tyr Ile Ala Lys His Tyr																				
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Trp	Phe	Val	Tyr	Phe	Ser	Leu	Ser	Leu	Lys	Asn	Ser	Leu	Glu	Met	Asp
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Ala	Glu	Asn	Asn	Pro	Lys	Lys	Arg	Tyr	Leu	Val	Arg	Trp	Glu	Arg	Met
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gca gtg gtt gtt tta ttt tta acg ctg gtt tta ttg ttt tta gtt tta 165
Ala Val Val Val Leu Phe Leu Thr Leu Val Leu Leu Phe Leu Val Leu
5 10 15

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atc gta ggg att ata gga gcg agc atc agc gtt tat act tac aag caa 261
Ile Val Gly Ile Ile Gly Ala Ser Ile Ser Val Tyr Thr Tyr Lys Gln
35 40 45 50

aac caa caa aac caa caa gag atc gct ttg caa aga gcg ttt tta agg 309
Asn Gln Gln Asn Gln Gln Glu Ile Ala Leu Gln Arg Ala Phe Leu Arg
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Asn Leu Val Ser Gly Thr Leu Ser Phe Leu Gly Lys Lys Gln Thr Pro
85 90 95

atg aaa gac gtt ctt gtg gat ttg gat tct tgt cag acg ctc caa aaa 453
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35 40 45
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50 55 60
Leu Arg Gly Glu Thr Leu Leu Cys Lys Gly Ile Lys Val Asn Asn Gln
65 70 75 80
Thr Phe Asn Leu Val Ser Gly Thr Leu Ser Phe Leu Gly Lys Lys Gln
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aaaccaacga aacc atg aaa aaa gct ctc tta cta act ctc tct ctc tcg 170
          Met Lys Lys Ala Leu Leu Leu Thr Leu Ser Leu Ser
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cta gaa gga agc tat att aaa gga caa ggt agc atc ggc aaa aaa gct 266
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30 35 40

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Ser	Ala	Glu	Asn	Ala	Leu	Asn	Glu	Ala	Ile	Asn	Asn	Ala	Lys	Asn	Ser	
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gca gtg aaa gat tca aac aaa atc gct agc cga ttc gca gga aat ggt 410
Ala Val Lys Asp Ser Asn Lys Ile Ala Ser Arg Phe Ala Gly Asn Gly
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gga tcg ggc ggt ctt ttt aat gag ctc agc ttt ggg tat aaa tat ttt 458
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qat aaq cga gcg tcc caa aaa tat gtt gaa cga agg gta aaa ggg ctc 650

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Ser Gln Lys Tyr	Val Glu Arg Arg Val	Lys Gly Leu Ser Ile Phe Tyr				
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Ser Arg His Val	Phe Arg Lys Ser	Ser Gly Leu Val Ile Gly Met Glu				
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Leu Gly Gly Ser	Thr Trp Phe Ala Ser	Asn Asn Leu Thr Pro Phe Asn				
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Arg Trp Asn Asn	Asp Glu Tyr Asp Ile	Asp Arg Tyr Gly Asp Glu Ile				
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Lys Val Asn Tyr	Tyr Ser Asp Asp Tyr	Gly Asp Lys Leu Asp Tyr Lys				
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gaa	atc	aag	ggt	tat	ggg	act	gaa	aag	gaa	aaa	gac	ggc	tta	aaa	tcc	411	
Glu	Ile	Lys	Gly	Tyr	Gly	Thr	Glu	Lys	Glu	Lys	Asp	Gly	Leu	Lys	Ser		
	75				80					85					90		
caa	atg	ggg	atc	aaa	aag	ggc	gac	acc	ttt	gat	gag	caa	aaa	tta	gag	459	
Gln	Met	Gly	Ile	Lys	Lys	Gly	Asp	Thr	Phe	Asp	Glu	Gln	Lys	Leu	Glu		
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cat	gct	aaa	acg	gct	tta	aaa	acc	gct	tta	gag	ggg	cag	ggc	tat	tat	507	
His	Ala	Lys	Thr	Ala	Leu	Lys	Thr	Ala	Leu	Glu	Gly	Gln	Gly	Tyr	Tyr		
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Ile	Gln	Asp	Val	Tyr	Met	Arg	Arg	Gly	Tyr	Leu	Asp	Ala	His	Ile	Ser		
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Tyr	Lys	Val	Lys	Glu	Gly	Ile	Gln	Tyr	Arg	Ile	Ser	Asp	Ile	Leu	Ile		
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Glu	Ile	Asp	Asn	Pro	Val	Val	Pro	Leu	Lys	Thr	Leu	Glu	Lys	Ala	Leu		
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aaa	gtg	aaa	agg	aaa	gat	gtc	ttt	aat	att	gag	cat	tta	aga	gcg	gat	987	
Lys	Val	Lys	Arg	Lys	Asp	Val	Phe	Asn	Ile	Glu	His	Leu	Arg	Ala	Asp		
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285 290 295	
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Val Val Lys Pro Asp Leu Asp Lys Asp Glu Lys Asn Gly Leu Val Lys	
300 305 310	
gtc att tat cgt att gaa gtg ggc gat atg gtg tat atc aat gat gtc	1131
Val Ile Tyr Arg Ile Glu Val Gly Asp Met Val Tyr Ile Asn Asp Val	
315 320 325 330	
atc att tca ggg aac cag cgc acg agc gat agg atc att aga agg gag	1179
Ile Ile Ser Gly Asn Gln Arg Thr Ser Asp Arg Ile Ile Arg Arg Glu	
335 340 345	
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Leu Leu Leu Gly Pro Lys Asp Lys Tyr Asn Leu Thr Lys Leu Arg Asn	
350 355 360	
tcc gaa aat tct tta agg cgt tta gga ttc ttc tct aaa gtc aaa att	1275
Ser Glu Asn Ser Leu Arg Arg Leu Gly Phe Phe Ser Lys Val Lys Ile	
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gaa gaa aaa agg gtt aat agc tca ctc atg gat tta tta gtg agc gta	1323
Glu Glu Lys Arg Val Asn Ser Ser Leu Met Asp Leu Leu Val Ser Val	
380 385 390	
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Glu Glu Gly Arg Thr Gly Gln Leu Gln Phe Gly Leu Gly Tyr Gly Ser	
395 400 405 410	
tat gga ggg ctt atg ctt aat ggg agc gtg agc gaa aga aac ctt ttt	1419
Tyr Gly Gly Leu Met Leu Asn Gly Ser Val Ser Glu Arg Asn Leu Phe	
415 420 425	
ggc aca ggg caa agc atg agc ttg tat gct aac atc gct aca ggg ggg	1467
Gly Thr Gly Gln Ser Met Ser Leu Tyr Ala Asn Ile Ala Thr Gly Gly	
430 435 440	
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Gly Arg Ser Tyr Pro Gly Met Pro Lys Gly Ala Gly Arg Met Phe Ala	
445 450 455	
ggg aat ttg agc ttg act aat cca agg att ttt gac agc tgg tat agc	1563
Gly Asn Leu Ser Leu Thr Asn Pro Arg Ile Phe Asp Ser Trp Tyr Ser	
460 465 470	
tct acg atc aac ctt tat gcg gat tac agg ata agc tac caa tac atc	1611
Ser Thr Ile Asn Leu Tyr Ala Asp Tyr Arg Ile Ser Tyr Gln Tyr Ile	
475 480 485 490	
caa caa ggc ggg ggc ttt ggg gtg aat gtc ggg cgc atg ctg ggt aat	1659
Gln Gln Gly Gly Gly Phe Gly Val Asn Val Gly Arg Met Leu Gly Asn	
495 500 505	
aga acc cat gtg agc tta ggg tat aac ttg aat gtt acc aaa ctc ctt	1707

Arg	Thr	His	Val	Ser	Leu	Gly	Tyr	Asn	Leu	Asn	Val	Thr	Lys	Leu	Leu		
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Gly	Phe	Ser	Ser	Pro	Leu	Tyr	Asn	Arg	Tyr	Tyr	Ser	Ser	Val	Asn	Glu		
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gtg	ggt	tct	cca	agg	caa	tgt	tct	acc	ccc	gca	tcg	gtg	att	atc	aat	1803	
Val	Val	Ser	Pro	Arg	Gln	Cys	Ser	Thr	Pro	Ala	Ser	Val	Ile	Ile	Asn		
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cgc	tta	tca	ggc	ggt	aaa	acc	ccc	tta	caa	cct	gaa	agc	tgt	tct	agt	1851	
Arg	Leu	Ser	Gly	Gly	Lys	Thr	Pro	Leu	Gln	Pro	Glu	Ser	Cys	Ser	Ser		
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cct	gga	gcg	atc	acc	act	tca	cca	gaa	ata	aga	ggt	att	tgg	gat	agg	1899	
Pro	Gly	Ala	Ile	Thr	Thr	Ser	Pro	Glu	Ile	Arg	Gly	Ile	Trp	Asp	Arg		
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gat	tac	cat	acg	cct	atc	acc	agc	tct	ttc	acc	ctt	gat	gtg	agc	tat	1947	
Asp	Tyr	His	Thr	Pro	Ile	Thr	Ser	Ser	Phe	Thr	Leu	Asp	Val	Ser	Tyr		
			590				595						600				
gac	aac	acc	gat	gat	tat	tac	ttc	cct	aga	aat	ggg	ggt	atc	ttt	agt	1995	
Asp	Asn	Thr	Asp	Asp	Tyr	Tyr	Phe	Pro	Arg	Asn	Gly	Val	Ile	Phe	Ser		
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tcc	tat	gcg	acg	atg	tct	ggc	ttg	cca	agc	tct	ggc	acg	ctc	aat	tct	2043	
Ser	Tyr	Ala	Thr	Met	Ser	Gly	Leu	Pro	Ser	Ser	Gly	Thr	Leu	Asn	Ser		
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tgg	aac	ggg	tta	ggc	ggg	aat	gtc	cgt	aac	acc	aaa	ggt	tat	ggt	aaa	2091	
Trp	Asn	Gly	Leu	Gly	Gly	Asn	Val	Arg	Asn	Thr	Lys	Val	Tyr	Gly	Lys		
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ttc	gcc	gct	tac	cac	cat	ttg	caa	aaa	tat	tta	ttg	ata	gat	ttg	atc	2139	
Phe	Ala	Ala	Tyr	His	His	Leu	Gln	Lys	Tyr	Leu	Leu	Ile	Asp	Leu	Ile		
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gct	cgc	ttt	aaa	acg	caa	gga	ggt	tat	atc	ttt	agg	tat	aac	acc	gat	2187	
Ala	Arg	Phe	Lys	Thr	Gln	Gly	Gly	Tyr	Ile	Phe	Arg	Tyr	Asn	Thr	Asp		
			670				675						680				
gat	tac	ttg	ccc	tta	aac	tcc	acc	ttc	tac	atg	ggg	ggc	gta	acc	acg	2235	
Asp	Tyr	Leu	Pro	Leu	Asn	Ser	Thr	Phe	Tyr	Met	Gly	Gly	Val	Thr	Thr		
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gtg	aga	ggc	ttt	agg	aac	gga	tcg	ggt	act	cct	aaa	gat	gag	ttt	ggc	2283	
Val	Arg	Gly	Phe	Arg	Asn	Gly	Ser	Val	Thr	Pro	Lys	Asp	Glu	Phe	Gly		
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ttg	tgg	ctt	gga	ggc	gat	ggg	att	ttt	acc	gct	tct	act	gaa	ttg	agc	2331	
Leu	Trp	Leu	Gly	Gly	Asp	Gly	Ile	Phe	Thr	Ala	Ser	Thr	Glu	Leu	Ser		
715					720					725					730		
tat	ggg	gtg	cta	aag	gcg	gct	aaa	atg	cgc	tta	gcg	tgg	ttt	ttt	gac	2379	
Tyr	Gly	Val	Leu	Lys	Ala	Ala	Lys	Met	Arg	Leu	Ala	Trp	Phe	Phe	Asp		
				735					740						745		

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Phe Gly Phe Leu Thr Phe Lys Thr Pro Thr Arg Gly Ser Phe Phe Tyr
750 755 760

aac gct cct gtt acg aca gcg aat ttt aaa gat tat ggc gtt ata ggg 2475
Asn Ala Pro Val Thr Thr Ala Asn Phe Lys Asp Tyr Gly Val Ile Gly
765 770 775

gct ggg ttt gaa aga gcg act tgg agg gct tcc aca ggc ttg cag att 2523
Ala Gly Phe Glu Arg Ala Thr Trp Arg Ala Ser Thr Gly Leu Gln Ile
780 785 790

gaa tgg att tcg ccc atg ggg cct ttg gtg ttg att ttc cct ata gcg 2571
Glu Trp Ile Ser Pro Met Gly Pro Leu Val Leu Ile Phe Pro Ile Ala
795 800 805 810

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Phe Phe Asn Gln Trp Gly Asp Gly Asn Gly Lys Lys Cys Lys Gly Leu
815 820 825

tgc ttc aac cct aac atg gac gat tac acg caa cac ttt gaa ttt tct 2667
Cys Phe Asn Pro Asn Met Asp Asp Tyr Thr Gln His Phe Glu Phe Ser
830 835 840

atg gga aca agg ttt taaaatgcgc atcaacagag aagaaatttt ggatttaatg 2722
Met Gly Thr Arg Phe
845

aaaaacgcgc ccttgaaaga attggggcaa agggcctttga ggggtgaagca acgcttgac 2782
cctgaaaact tgacgacttt tattgtggat aggaatatca attacaccaa tattgtttt 2842
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agctatgaag aaattgatca aaagattgaa gaattgctcg ctattggcgg cacgcagatc 2962
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<213> Helicobacter pylori

<400> 8

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Ser Lys Lys Ile Asp Thr Ala Val Leu Ala Leu Phe Asn Gln Gly Tyr
35 40 45
Phe Lys Asp Val Tyr Ala Thr Phe Glu Gly Gly Ile Leu Glu Phe His
50 55 60
Phe Asp Glu Lys Ala Arg Ile Ala Gly Val Glu Ile Lys Gly Tyr Gly
65 70 75 80
Thr Glu Lys Glu Lys Asp Gly Leu Lys Ser Gln Met Gly Ile Lys Lys
85 90 95
Gly Asp Thr Phe Asp Glu Gln Lys Leu Glu His Ala Lys Thr Ala Leu
100 105 110
Lys Thr Ala Leu Glu Gly Gln Gly Tyr Tyr Gly Ser Val Val Glu Val
115 120 125
Arg Thr Glu Lys Val Ser Glu Gly Ala Leu Leu Ile Val Phe Asp Val

130	Asn	Arg	Gly	Asp	Ser	Ile	Tyr	Ile	Lys	Gln	Ser	Ile	Tyr	Glu	Gly	Ser
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	Leu	Asp	Gln	Leu	Glu	Tyr	Asp	Ser	Met	Arg	Ile	Gln	Asp	Val	Tyr	Met
	Arg	Arg	Gly	Tyr	Leu	Asp	Ala	His	Ile	Ser	Ser	Pro	Phe	Leu	Lys	Thr
	Asp	Phe	Ser	Thr	His	Asp	Ala	Lys	Leu	His	Tyr	Lys	Val	Lys	Glu	Gly
	Ile	Gln	Tyr	Arg	Ile	Ser	Asp	Ile	Leu	Ile	Glu	Ile	Asp	Asn	Pro	Val
	Val	Pro	Leu	Lys	Thr	Leu	Glu	Lys	Ala	Leu	Lys	Val	Lys	Arg	Lys	Asp
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	Glu	Ile	Ala	Asp	Lys	Gly	Tyr	Ala	Phe	Ala	Val	Val	Lys	Pro	Asp	Leu
	Asp	Lys	Asp	Glu	Lys	Asn	Gly	Leu	Val	Lys	Val	Ile	Tyr	Arg	Ile	Glu
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	Asp	Lys	Tyr	Asn	Leu	Thr	Lys	Leu	Arg	Asn	Ser	Glu	Asn	Ser	Leu	Arg
	Arg	Leu	Gly	Phe	Phe	Ser	Lys	Val	Lys	Ile	Glu	Glu	Lys	Arg	Val	Asn
	Ser	Ser	Leu	Met	Asp	Leu	Leu	Val	Ser	Val	Glu	Glu	Gly	Arg	Thr	Gly
	Gln	Leu	Gln	Phe	Gly	Leu	Gly	Tyr	Gly	Ser	Tyr	Gly	Gly	Leu	Met	Leu
	Asn	Gly	Ser	Val	Ser	Glu	Arg	Asn	Leu	Phe	Gly	Thr	Gly	Gln	Ser	Met
	Ser	Leu	Tyr	Ala	Asn	Ile	Ala	Thr	Gly	Gly	Gly	Arg	Ser	Tyr	Pro	Gly
	Met	Pro	Lys	Gly	Ala	Gly	Arg	Met	Phe	Ala	Gly	Asn	Leu	Ser	Leu	Thr
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	Ala	Asp	Tyr	Arg	Ile	Ser	Tyr	Gln	Tyr	Ile	Gln	Gln	Gly	Gly	Gly	Phe
	Gly	Val	Asn	Val	Gly	Arg	Met	Leu	Gly	Asn	Arg	Thr	His	Val	Ser	Leu
	Gly	Tyr	Asn	Leu	Asn	Val	Thr	Lys	Leu	Leu	Gly	Phe	Ser	Ser	Pro	Leu
	Tyr	Asn	Arg	Tyr	Tyr	Ser	Ser	Val	Asn	Glu	Val	Val	Ser	Pro	Arg	Gln
	Cys	Ser	Thr	Pro	Ala	Ser	Val	Ile	Ile	Asn	Arg	Leu	Ser	Gly	Gly	Lys
	Thr	Pro	Leu	Gln	Pro	Glu	Ser	Cys	Ser	Ser	Pro	Gly	Ala	Ile	Thr	Thr
	Ser	Pro	Glu	Ile	Arg	Gly	Ile	Trp	Asp	Arg	Asp	Tyr	His	Thr	Pro	Ile
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Glu	Glu	Ser	Ile	Gly	Ile	Ser	Ile	Leu	Gln	Met	Ala	Leu	Ser	Ser	Phe	
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gtg	ggc	tct	ggt	ttg	aat	ttc	aaa	aaa	aaa	tcg	ctt	gat	ttt	tct	tta	364
Val	Gly	Ser	Val	Leu	Asn	Phe	Lys	Lys	Lys	Ser	Leu	Asp	Phe	Ser	Leu	
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ggc	ttg	ttg	ata	ggg	gca	ggg	ggg	ctg	ata	ggg	gcg	agt	ttt	agc	gga	412
Gly	Leu	Leu	Ile	Gly	Ala	Gly	Gly	Leu	Ile	Gly	Ala	Ser	Phe	Ser	Gly	
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ttt	ggt	tta	aaa	atc	ggt	tcc	agt	aaa	att	tta	atg	ggt	att	ttc	gcg	460
Phe	Val	Leu	Lys	Ile	Val	Ser	Ser	Lys	Ile	Leu	Met	Val	Ile	Phe	Ala	
				90				95				100				
ctt	tta	gtc	gtg	tat	tct	atg	atc	caa	ttt	ggt	ttg	aaa	ccc	aaa	aaa	508
Leu	Leu	Val	Val	Tyr	Ser	Met	Ile	Gln	Phe	Val	Leu	Lys	Pro	Lys	Lys	
105						110					115				120	
aaa	gat	ttg	ata	gcg	gat	act	aaa	cgc	tat	cat	ctg	caa	ggt	ttg	aaa	556
Lys	Asp	Leu	Ile	Ala	Asp	Thr	Lys	Arg	Tyr	His	Leu	Gln	Gly	Leu	Lys	
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Leu	Phe	Leu	Ile	Gly	Thr	Leu	Thr	Gly	Phe	Phe	Ala	Ile	Thr	Leu	Gly	
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att	ggt	ggg	ggg	atg	ctc	atg	gtg	cct	ttg	atg	cat	tat	ttt	tta	ggg	652
Ile	Gly	Gly	Gly	Met	Leu	Met	Val	Pro	Leu	Met	His	Tyr	Phe	Leu	Gly	
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tat	gat	tct	aaa	aaa	tgc	gtg	gct	cta	ggg	tta	ttt	ttc	atc	ttg	ttt	700
Tyr	Asp	Ser	Lys	Lys	Cys	Val	Ala	Leu	Gly	Leu	Phe	Phe	Ile	Leu	Phe	
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tct	tct	att	tca	gga	gct	ttt	tct	tta	atg	tat	cac	cac	atc	atc	aat	748
Ser	Ser	Ile	Ser	Gly	Ala	Phe	Ser	Leu	Met	Tyr	His	His	Ile	Ile	Asn	
185						190					195				200	
aaa	gaa	gtg	ctc	tta	gca	ggg	gcg	att	gtg	gga	tta	gga	tct	ggt	atg	796
Lys	Glu	Val	Leu	Leu	Ala	Gly	Ala	Ile	Val	Gly	Leu	Gly	Ser	Val	Met	
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ggc	gtg	agc	att	ggg	att	aaa	tgg	atc	atg	ggg	ctt	ttg	aat	gaa	aaa	844
Gly	Val	Ser	Ile	Gly	Ile	Lys	Trp	Ile	Met	Gly	Leu	Leu	Asn	Glu	Lys	
				220				225					230			
atg	cat	aaa	gct	ttg	att	tta	ggg	gtg	tat	ggt	ttg	tcg	cta	ttg	att	892
Met	His	Lys	Ala	Leu	Ile	Leu	Gly	Val	Tyr	Gly	Leu	Ser	Leu	Leu	Ile	
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Val	Leu	Tyr	Lys	Leu	Phe	Phe										
				250			255									
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 Met Leu Ala Thr Gly His Ser Phe Glu Glu Ser Ile Gly Ile Ser Ile
 35 40 45
 Leu Gln Met Ala Leu Ser Ser Phe Val Gly Ser Val Leu Asn Phe Lys
 50 55 60
 Lys Lys Ser Leu Asp Phe Ser Leu Gly Leu Leu Ile Gly Ala Gly Gly
 65 70 75 80
 Leu Ile Gly Ala Ser Phe Ser Gly Phe Val Leu Lys Ile Val Ser Ser
 85 90 95
 Lys Ile Leu Met Val Ile Phe Ala Leu Leu Val Val Tyr Ser Met Ile
 100 105 110
 Gln Phe Val Leu Lys Pro Lys Lys Lys Asp Leu Ile Ala Asp Thr Lys
 115 120 125
 Arg Tyr His Leu Gln Gly Leu Lys Leu Phe Leu Ile Gly Thr Leu Thr
 130 135 140
 Gly Phe Phe Ala Ile Thr Leu Gly Ile Gly Gly Gly Met Leu Met Val
 145 150 155 160
 Pro Leu Met His Tyr Phe Leu Gly Tyr Asp Ser Lys Lys Cys Val Ala
 165 170 175
 Leu Gly Leu Phe Phe Ile Leu Phe Ser Ser Ile Ser Gly Ala Phe Ser
 180 185 190
 Leu Met Tyr His His Ile Ile Asn Lys Glu Val Leu Leu Ala Gly Ala
 195 200 205
 Ile Val Gly Leu Gly Ser Val Met Gly Val Ser Ile Gly Ile Lys Trp
 210 215 220
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 Met Gly Arg Ile Glu Ser Lys Lys Arg Leu Lys Ala Leu Val Phe
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Phe Phe Lys Thr 35 Lys Asn His Ile Tyr 40 Leu Gly Phe Arg Leu Gly Thr 45	
gga gcc aat gtg cac acg agc atg tgg caa caa gcc tat aaa gac aac	254
Gly Ala Asn Val 50 His Thr Ser Met 55 Trp Gln Gln Ala Tyr 60 Lys Asp Asn	
ccc acc tgc cct ggt agc gtg tgt tat ggc gag aaa tta gaa gcc cat	302
Pro Thr Cys Pro Gly Ser Val Cys Tyr Gly Glu Lys Leu Glu Ala His 75	
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Tyr Gln Gly Gly Lys Asn Leu Ser Tyr Thr 80 85 90 Gln Ile Gly Asp Glu 95	
ata gct ttt gat aaa cac cat att tta ggc tta agg gtg tgg ggg gat	398
Ile Ala Phe Asp 100 Lys His His Ile Leu Gly Leu Arg Val Trp Gly Asp 110	
gta gaa tac gct aaa gcg caa tta ggt caa aaa gtg ggg ggt aat acc	446
Val Glu Tyr Ala Lys Ala Gln Leu Gly Gln Lys Val Gly Gly Asn Thr 115 120 125	
ctt tta tcc caa gcc aat tat gac cca aac gcg att aaa acc tac gat	494
Leu Leu Ser Gln Ala Asn Tyr Asp Pro Asn Ala Ile Lys Thr Tyr Asp 130 135 140	
tct gct tca aac act caa ggc cct tta gtt ttg caa aaa acc cca agc	542
Ser Ala Ser Asn Thr Gln Gly Pro Leu Val Leu Gln Lys Thr Pro Ser 145 150 155	
cct caa aac ttc ctt ttc aat aac ggg cat ttc atg gcg ttt ggt ttg	590
Pro Gln Asn Phe Leu Phe Asn Asn Gly His Phe Met Ala Phe Gly Leu 160 165 170 175	
aac gtg aat gtg ttt gtt aac ctc cct ata gac acc ctt tta aaa ctc	638
Asn Val Asn Val Phe Val Asn Leu Pro Ile Asp Thr Leu Leu Lys Leu 180 185 190	
gct tta aaa aca gaa aaa atg ctg ttt ttt aaa ata ggc gtg ttt ggt	686
Ala Leu Lys Thr 195 Glu Lys Met Leu Phe Phe Lys Ile Gly Val Phe Gly 200 205	
ggg ggc ggg gtg gaa tac gca ata tta tgg agt cct aac tat caa aat	734
Gly Gly Gly Val Glu Tyr Ala Ile Leu Trp Ser Pro Asn Tyr Gln Asn 210 215 220	
caa aac acg aaa caa ggc gat aaa ttt ttt gca gcg ggt ggg ggg ttt	782
Gln Asn Thr Lys Gln Gly Asp Lys Phe Phe Ala Ala Gly Gly Gly Phe 225 230 235	
ttt gtg aat ttt ggg ggt tct ttg tat ata ggc aaa cgc aac cgc ttc	830
Phe Val Asn Phe Gly Gly Ser Leu Tyr Ile Gly Lys Arg Asn Arg Phe 240 245 250 255	
aat gtg ggg tta aaa atc cct tac tat agc ttg agc gcg caa agt tgg	878

Asn Val Gly Leu Lys Ile Pro Tyr Tyr Ser Leu Ser Ala Gln Ser Trp
 260 265 270

aaa aac ttt ggc tct agc aat gtg tgg cag caa caa acg atc cga caa 926
 Lys Asn Phe Gly Ser Ser Asn Val Trp Gln Gln Gln Thr Ile Arg Gln
 275 280 285

aac ttc agc gtt ttt agg aat aaa gaa gtt ttt gtc agc tac gcg ttc 974
 Asn Phe Ser Val Phe Arg Asn Lys Glu Val Phe Val Ser Tyr Ala Phe
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 Ala Asn Val His Thr Ser Met Trp Gln Gln Ala Tyr Lys Asp Asn Pro
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 Thr Cys Pro Gly Ser Val Cys Tyr Gly Glu Lys Leu Glu Ala His Tyr
 65 70 75 80
 Gln Gly Gly Lys Asn Leu Ser Tyr Thr Gly Gln Ile Gly Asp Glu Ile
 85 90 95
 Ala Phe Asp Lys His His Ile Leu Gly Leu Arg Val Trp Gly Asp Val
 100 105 110
 Glu Tyr Ala Lys Ala Gln Leu Gly Gln Lys Val Gly Gly Asn Thr Leu
 115 120 125
 Leu Ser Gln Ala Asn Tyr Asp Pro Asn Ala Ile Lys Thr Tyr Asp Ser
 130 135 140
 Ala Ser Asn Thr Gln Gly Pro Leu Val Leu Gln Lys Thr Pro Ser Pro
 145 150 155 160
 Gln Asn Phe Leu Phe Asn Asn Gly His Phe Met Ala Phe Gly Leu Asn
 165 170 175
 Val Asn Val Phe Val Asn Leu Pro Ile Asp Thr Leu Leu Lys Leu Ala
 180 185 190
 Leu Lys Thr Glu Lys Met Leu Phe Phe Lys Ile Gly Val Phe Gly Gly
 195 200 205
 Gly Gly Val Glu Tyr Ala Ile Leu Trp Ser Pro Asn Tyr Gln Asn Gln
 210 215 220
 Asn Thr Lys Gln Gly Asp Lys Phe Phe Ala Ala Gly Gly Gly Phe Phe
 225 230 235 240
 Val Asn Phe Gly Gly Ser Leu Tyr Ile Gly Lys Arg Asn Arg Phe Asn
 245 250 255
 Val Gly Leu Lys Ile Pro Tyr Tyr Ser Leu Ser Ala Gln Ser Trp Lys
 260 265 270
 Asn Phe Gly Ser Ser Asn Val Trp Gln Gln Gln Thr Ile Arg Gln Asn

taaaaaatgg aatatcccaa cgattttcgt tttcaccaac acacaagaaa aagccggcga 605
 tgcctttgtt aaaaaaact 624

<210> 14
 <211> 153
 <212> PRT
 <213> Helicobacter pylori

<400> 14
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 1 5 10 15
 Phe Leu Gly Asp Ala Phe Thr Leu Asp Gly Lys Glu Gly Gly Leu Asn
 20 25 30
 Met Glu Lys Leu Arg Glu Ala Ile Lys Lys Glu Lys Pro Ile Met Asn
 35 40 45
 Ile Leu Leu Met Gly Ala Thr Gly Val Gly Lys Ser Ser Leu Ile Asn
 50 55 60
 Ala Leu Phe Gly Lys Glu Val Ala Lys Ala Gly Val Gly Lys Pro Ile
 65 70 75 80
 Thr Gln His Leu Glu Lys Tyr Val Asp Glu Glu Lys Gly Leu Ile Leu
 85 90 95
 Trp Asp Thr Lys Gly Ile Glu Asp Lys Asp Tyr Glu Asn Thr Leu Glu
 100 105 110
 Ser Ile Lys Lys Glu Met Glu Asp Ser Phe Lys Thr Leu Asp Glu Lys
 115 120 125
 Glu Ala Ile Asp Val Ala Tyr Leu Cys Val Lys Glu Thr Ser Gly Arg
 130 135 140
 Val Gln Glu Arg Glu Arg Glu Ser Tyr
 145 150

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 <211> 1083
 <212> DNA
 <213> Helicobacter pylori

<220>
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 <222> (155)...(1033)

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 gataaaggga gtgtagtag atagtttttaa taggggttatt gactatatta gggtttctgt 120
 aaccaaacag tgcaatttca ggtgtcagta ttgc atg cct gct acg cca tta aat 175
 Met Pro Ala Thr Pro Leu Asn
 1 5
 ttt ttt gat aat gaa gaa tta ttg cct ttg gat aat gtt tta gaa ttt 223
 Phe Phe Asp Asn Glu Glu Leu Leu Pro Leu Asp Asn Val Leu Glu Phe
 10 15 20
 ctc aaa atc gcc att gat gag ggc gtt aaa aaa att aga atc acg ggt 271
 Leu Lys Ile Ala Ile Asp Glu Gly Val Lys Lys Ile Arg Ile Thr Gly
 25 30 35
 ggg gag ccg cta tta cgc aaa ggc tta gat gaa ttt atc gct aaa ttg 319
 Gly Glu Pro Leu Leu Arg Lys Gly Leu Asp Glu Phe Ile Ala Lys Leu
 40 45 50 55

cac gct tac aat aaa gaa gtg gag tta gtt tta agc act aat ggt ttt	367
His Ala Tyr Asn Lys Glu Val Glu Leu Val Leu Ser Thr Asn Gly Phe	
60 65 70	
tta ctc aaa aaa atg gct aag gat tta aaa aat gcc ggg tta gcg caa	415
Leu Leu Lys Lys Met Ala Lys Asp Leu Lys Asn Ala Gly Leu Ala Gln	
75 80 85	
gtg aat gtt tca ttg gat tct tta aaa agc gat agg gtt tta aaa atc	463
Val Asn Val Ser Leu Asp Ser Leu Lys Ser Asp Arg Val Leu Lys Ile	
90 95 100	
tct caa aaa gac gct ctt aaa aac acg cta gaa ggg att gaa gag tct	511
Ser Gln Lys Asp Ala Leu Lys Asn Thr Leu Glu Gly Ile Glu Glu Ser	
105 110 115	
ttg aaa gtg ggt tta aaa ctc aaa tta aac acg gtt gtg ata aaa agc	559
Leu Lys Val Gly Leu Lys Leu Lys Leu Asn Thr Val Val Ile Lys Ser	
120 125 130 135	
ggt aat gat gat gaa atc tta gag ctt tta gaa tac gca aaa aat agg	607
Val Asn Asp Asp Glu Ile Leu Glu Leu Glu Tyr Ala Lys Asn Arg	
140 145 150	
cat ata caa atc cgc tac att gaa ttt atg gaa aac acg cat gct aaa	655
His Ile Gln Ile Arg Tyr Ile Glu Phe Met Glu Asn Thr His Ala Lys	
155 160 165	
agt ttg gtt aaa ggc ttg aaa gag cga gaa att tta gat ttg atc gct	703
Ser Leu Val Lys Gly Leu Lys Glu Arg Glu Ile Leu Asp Leu Ile Ala	
170 175 180	
caa aaa tat caa atc att gag gca gaa aaa ccc aaa caa ggg tct tct	751
Gln Lys Tyr Gln Ile Ile Glu Ala Glu Lys Pro Lys Gln Gly Ser Ser	
185 190 195	
aaa atc tac acg cta gaa aat ggc tat caa ttt ggc att atc gct ccg	799
Lys Ile Tyr Thr Leu Glu Asn Gly Tyr Gln Phe Gly Ile Ile Ala Pro	
200 205 210 215	
cat agc gat gat ttt tgc caa tct tgc aat cgt atc cgt ttg gct tct	847
His Ser Asp Asp Phe Cys Gln Ser Cys Asn Arg Ile Arg Leu Ala Ser	
220 225 230	
gat ggt aag att tgc cca tgt tta tac tat caa gac gcc ata gac gct	895
Asp Gly Lys Ile Cys Pro Cys Leu Tyr Tyr Gln Asp Ala Ile Asp Ala	
235 240 245	
aaa gag gcg atc atc aat aag gat aca aaa aat ata aaa agg ctt tta	943
Lys Glu Ala Ile Ile Asn Lys Asp Thr Lys Asn Ile Lys Arg Leu Leu	
250 255 260	
aag caa tct gtc atc aat aaa cca gaa aaa aac atg tgg aat gat aaa	991
Lys Gln Ser Val Ile Asn Lys Pro Glu Lys Asn Met Trp Asn Asp Lys	
265 270 275	
aac agc gaa act ccc aca agg gcg ttt tac tac aca ggg ggg	1033

Asn Ser Glu Thr Pro Thr Arg Ala Phe Tyr Tyr Thr Gly Gly
 280 285 290

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1083

<210> 16

<211> 293

<212> PRT

<213> Helicobacter pylori

<400> 16

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			20					25					30		
Lys	Lys	Ile	Arg	Ile	Thr	Gly	Gly	Glu	Pro	Leu	Leu	Arg	Lys	Gly	Leu
		35				40						45			
Asp	Glu	Phe	Ile	Ala	Lys	Leu	His	Ala	Tyr	Asn	Lys	Glu	Val	Glu	Leu
	50					55					60				
Val	Leu	Ser	Thr	Asn	Gly	Phe	Leu	Leu	Lys	Lys	Met	Ala	Lys	Asp	Leu
65					70					75				80	
Lys	Asn	Ala	Gly	Leu	Ala	Gln	Val	Asn	Val	Ser	Leu	Asp	Ser	Leu	Lys
				85					90					95	
Ser	Asp	Arg	Val	Leu	Lys	Ile	Ser	Gln	Lys	Asp	Ala	Leu	Lys	Asn	Thr
			100					105						110	
Leu	Glu	Gly	Ile	Glu	Glu	Ser	Leu	Lys	Val	Gly	Leu	Lys	Leu	Lys	Leu
			115					120					125		
Asn	Thr	Val	Val	Ile	Lys	Ser	Val	Asn	Asp	Asp	Glu	Ile	Leu	Glu	Leu
	130					135					140				
Leu	Glu	Tyr	Ala	Lys	Asn	Arg	His	Ile	Gln	Ile	Arg	Tyr	Ile	Glu	Phe
145					150					155					160
Met	Glu	Asn	Thr	His	Ala	Lys	Ser	Leu	Val	Lys	Gly	Leu	Lys	Glu	Arg
				165					170					175	
Glu	Ile	Leu	Asp	Leu	Ile	Ala	Gln	Lys	Tyr	Gln	Ile	Ile	Glu	Ala	Glu
			180					185					190		
Lys	Pro	Lys	Gln	Gly	Ser	Ser	Lys	Ile	Tyr	Thr	Leu	Glu	Asn	Gly	Tyr
		195					200						205		
Gln	Phe	Gly	Ile	Ile	Ala	Pro	His	Ser	Asp	Asp	Phe	Cys	Gln	Ser	Cys
	210					215					220				
Asn	Arg	Ile	Arg	Leu	Ala	Ser	Asp	Gly	Lys	Ile	Cys	Pro	Cys	Leu	Tyr
225					230					235					240
Tyr	Gln	Asp	Ala	Ile	Asp	Ala	Lys	Glu	Ala	Ile	Ile	Asn	Lys	Asp	Thr
			245						250					255	
Lys	Asn	Ile	Lys	Arg	Leu	Leu	Lys	Gln	Ser	Val	Ile	Asn	Lys	Pro	Glu
			260					265					270		
Lys	Asn	Met	Trp	Asn	Asp	Lys	Asn	Ser	Glu	Thr	Pro	Thr	Arg	Ala	Phe
		275					280						285		
Tyr	Tyr	Thr	Gly	Gly											
	290														

<210> 17

<211> 1181

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (121)...(1137)

<400> 17

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atg agc gga	tcg aat caa	ggg tgg gaa	gtg tat tat	cag ccc tat	aag	168
Met Ser Gly	Ser Asn Gln	Gly Trp Glu	Val Tyr Tyr	Gln Pro Tyr	Lys	
1	5	10	15			
act gaa acg	caa agg tta	agg ttt tgg	tgg tgg agt	tct ttt ggg	aga	216
Thr Glu Thr	Gln Arg Leu	Arg Phe Trp	Trp Trp Trp	Ser Ser Phe	Gly Arg	
	20	25	30			
ggc tta gcg	ttc aac tct	tgg att tat	gag ttt ttt	gcg acg gtg	cct	264
Gly Leu Ala	Phe Asn Ser	Trp Ile Tyr	Glu Phe Phe	Ala Thr Val	Pro	
	35	40	45			
tat ttg aaa	aag gga ggc	aat cct aat	aac agc aac	gat ttc atc	aat	312
Tyr Leu Lys	Lys Gly Gly	Asn Pro Asn	Asn Ser Asn	Asp Phe Ile	Asn	
	50	55	60			
tat ggc tgg	cat gga atc	acc aca acc	tat tct tat	aaa ggt tta	gac	360
Tyr Gly Trp	His Gly Ile	Thr Thr Thr	Tyr Ser Tyr	Lys Gly Leu	Asp	
	65	70	75		80	
gct caa ttt	ttt tat tat	ttt gcg cct	aag act tat	aac gct cct	ggc	408
Ala Gln Phe	Phe Tyr Tyr	Phe Ala Pro	Lys Thr Tyr	Asn Ala Pro	Gly	
	85	90	95			
ttt aag ctg	gtc tat gac	acg aat agg	aat ttt caa	aat gta ggc	ttt	456
Phe Lys Leu	Val Tyr Asp	Thr Asn Arg	Asn Phe Gln	Asn Val Gly	Phe	
	100	105	110			
cgc tct caa	agc atg atc	atg aca acc	ttt cct tta	tac tat aga	ggg	504
Arg Ser Gln	Ser Met Ile	Met Thr Thr	Phe Pro Leu	Tyr Tyr Arg	Gly	
	115	120	125			
tgg tat aac	cca gag aca	aac act tat	agt tta gaa	gac agc acg	cct	552
Trp Tyr Asn	Pro Glu Thr	Asn Thr Tyr	Ser Leu Glu	Asp Ser Thr	Pro	
	130	135	140			
cat ggc tcg	ttg ttg ggg	agg aat ggc	gtt act tta	aat atc cgc	cag	600
His Gly Ser	Leu Leu Gly	Arg Asn Gly	Val Thr Leu	Asn Ile Arg	Gln	
	145	150	155		160	
gtt ttt tgg	tgg gat aat	ttc aac tgg	tcc att ggc	ttt tat aac	acc	648
Val Phe Trp	Trp Asp Asn	Phe Asn Trp	Ser Ile Gly	Phe Tyr Asn	Thr	
	165	170	175			
ttt ggc aat	tcg gac gct	ttt tta ggc	tct cac acg	atg cca agg	ggc	696
Phe Gly Asn	Ser Asp Ala	Phe Leu Gly	Ser His Thr	Met Pro Arg	Gly	
	180	185	190			
aat aac act	tcc tat atc	ggc agt gaa	atc tcc ata	acg act agg	cat	744
Asn Asn Thr	Ser Tyr Ile	Gly Ser Glu	Ile Ser Ile	Thr Thr Arg	His	
	195	200	205			
gcc gga atg	att ggc tat	gat ttt tgg	gat aat acg	gct tat gat	ggg	792

Ala Gly Met Ile Gly Tyr Asp Phe Trp Asp Asn Thr Ala Tyr Asp Gly	
210 215 220	
cta gct gat gcg atc act aac gct aac act ttc act ttt tac act tct	840
Leu Ala Asp Ala Ile Thr Asn Ala Asn Thr Phe Thr Phe Tyr Thr Ser	
225 230 235 240	
gtt gga ggg atc cat aag cgt ttt gca tgg cat gtt ttt ggg cgc gtc	888
Val Gly Gly Ile His Lys Arg Phe Ala Trp His Val Phe Gly Arg Val	
245 250 255	
tct cat gcg aat aaa aac gcg tta ggg caa gtg ggg agg gct aat gaa	936
Ser His Ala Asn Lys Asn Ala Leu Gly Gln Val Gly Arg Ala Asn Glu	
260 265 270	
tat tcc ttg caa ttc aac gcg agc tat gcg ttc act gaa tca atc ctt	984
Tyr Ser Leu Gln Phe Asn Ala Ser Tyr Ala Phe Thr Glu Ser Ile Leu	
275 280 285	
ctt aac ttt agg atc act tat tat ggg gct agg atc aat aaa ggg tat	1032
Leu Asn Phe Arg Ile Thr Tyr Tyr Gly Ala Arg Ile Asn Lys Gly Tyr	
290 295 300	
caa gcg ggg tat ttt gga gcg ccc aaa ttc aat aac cct gat ggc gat	1080
Gln Ala Gly Tyr Phe Gly Ala Pro Lys Phe Asn Asn Pro Asp Gly Asp	
305 310 315 320	
ttt agc gct aat tac caa gac aga agt tac atg atg acc aac ctc acg	1128
Phe Ser Ala Asn Tyr Gln Asp Arg Ser Tyr Met Met Thr Asn Leu Thr	
325 330 335	
ctg aag ttt tgattttccaa tcacagcgag ttaaaaacac tccaaggcat	1177
Leu Lys Phe	

tttt 1181

<210> 18
 <211> 339
 <212> PRT
 <213> Helicobacter pylori

<400> 18

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Gly Leu Ala Phe Asn Ser Trp Ile Tyr Glu Phe Phe Ala Thr Val Pro	
35 40 45	
Tyr Leu Lys Lys Gly Gly Asn Pro Asn Asn Ser Asn Asp Phe Ile Asn	
50 55 60	
Tyr Gly Trp His Gly Ile Thr Thr Thr Tyr Ser Tyr Lys Gly Leu Asp	
65 70 75 80	
Ala Gln Phe Phe Tyr Tyr Phe Ala Pro Lys Thr Tyr Asn Ala Pro Gly	
85 90 95	
Phe Lys Leu Val Tyr Asp Thr Asn Arg Asn Phe Gln Asn Val Gly Phe	
100 105 110	
Arg Ser Gln Ser Met Ile Met Thr Thr Phe Pro Leu Tyr Tyr Arg Gly	

	115		120		125										
Trp	Tyr	Asn	Pro	Glu	Thr	Asn	Thr	Tyr	Ser	Leu	Glu	Asp	Ser	Thr	Pro
	130					135					140				
His	Gly	Ser	Leu	Leu	Gly	Arg	Asn	Gly	Val	Thr	Leu	Asn	Ile	Arg	Gln
145					150						155				160
Val	Phe	Trp	Trp	Asp	Asn	Phe	Asn	Trp	Ser	Ile	Gly	Phe	Tyr	Asn	Thr
				165					170					175	
Phe	Gly	Asn	Ser	Asp	Ala	Phe	Leu	Gly	Ser	His	Thr	Met	Pro	Arg	Gly
			180					185					190		
Asn	Asn	Thr	Ser	Tyr	Ile	Gly	Ser	Glu	Ile	Ser	Ile	Thr	Thr	Arg	His
		195					200					205			
Ala	Gly	Met	Ile	Gly	Tyr	Asp	Phe	Trp	Asp	Asn	Thr	Ala	Tyr	Asp	Gly
	210					215					220				
Leu	Ala	Asp	Ala	Ile	Thr	Asn	Ala	Asn	Thr	Phe	Thr	Phe	Tyr	Thr	Ser
225					230					235					240
Val	Gly	Gly	Ile	His	Lys	Arg	Phe	Ala	Trp	His	Val	Phe	Gly	Arg	Val
				245					250					255	
Ser	His	Ala	Asn	Lys	Asn	Ala	Leu	Gly	Gln	Val	Gly	Arg	Ala	Asn	Glu
			260					265					270		
Tyr	Ser	Leu	Gln	Phe	Asn	Ala	Ser	Tyr	Ala	Phe	Thr	Glu	Ser	Ile	Leu
		275					280					285			
Leu	Asn	Phe	Arg	Ile	Thr	Tyr	Tyr	Gly	Ala	Arg	Ile	Asn	Lys	Gly	Tyr
	290					295					300				
Gln	Ala	Gly	Tyr	Phe	Gly	Ala	Pro	Lys	Phe	Asn	Asn	Pro	Asp	Gly	Asp
305					310				315						320
Phe	Ser	Ala	Asn	Tyr	Gln	Asp	Arg	Ser	Tyr	Met	Met	Thr	Asn	Leu	Thr
			325						330					335	
Leu	Lys	Phe													

<210> 19
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 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (133)...(879)

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 taataactttt ttagttataa taacaatttt gttttttcaa aaacaataat tactatatatt 120
 aggatttttaa ga atg aat gac aag cgt ttt aga aaa tat tgt agt ttt tct 171
 Met Asn Asp Lys Arg Phe Arg Lys Tyr Cys Ser Phe Ser
 1 5 10

att ttt ttg tcc tta tta gga acg ttt gaa tta gag gct aaa gaa gaa 219
 Ile Phe Leu Ser Leu Leu Gly Thr Phe Glu Leu Glu Ala Lys Glu Glu
 15 20 25

gaa gaa aaa gaa gaa aga aag aca gaa agg aaa aaa gaa aag aac gcc 267
 Glu Glu Lys Glu Glu Arg Lys Thr Glu Arg Lys Lys Glu Lys Asn Ala
 30 35 40 45

caa cac act cta ggc aag gtt acc act caa gcg gct aaa atc ttt aac 315
 Gln His Thr Leu Gly Lys Val Thr Thr Gln Ala Ala Lys Ile Phe Asn
 50 55 60

tac aac aac cag aca acc att tca agt aag gaa tta gaa aga agg caa	363
Tyr Asn Asn Gln Thr Thr Ile Ser Ser Lys Glu Leu Glu Arg Arg Gln	
65 70 75	
gcc aac caa atc agc gac atg ttt aga aga aac cct aat atc aat gtg	411
Ala Asn Gln Ile Ser Asp Met Phe Arg Arg Asn Pro Asn Ile Asn Val	
80 85 90	
ggc ggt ggt gcg gtg ata gcg caa aaa att tat gtg cgc ggt att gaa	459
Gly Gly Gly Ala Val Ile Ala Gln Lys Ile Tyr Val Arg Gly Ile Glu	
95 100 105	
gac aga ttg gct cgg gtt acg gtg gat ggg gcg gcg caa atg ggt gca	507
Asp Arg Leu Ala Arg Val Thr Val Asp Gly Ala Ala Gln Met Gly Ala	
110 115 120 125	
agc tat ggg cat caa ggc aat acg atc att gac cct gga atg ctt aaa	555
Ser Tyr Gly His Gln Gly Asn Thr Ile Ile Asp Pro Gly Met Leu Lys	
130 135 140	
agc gtg gtg gtt act aaa ggg gcg gct caa gcg agc gcg ggg cct atg	603
Ser Val Val Val Thr Lys Gly Ala Ala Gln Ala Ser Ala Gly Pro Met	
145 150 155	
gct ttg att ggc gcg att aaa atg gag act aaa agt gct agc gat ttt	651
Ala Leu Ile Gly Ala Ile Lys Met Glu Thr Lys Ser Ala Ser Asp Phe	
160 165 170	
atc cct aaa ggt aaa gac tac gcc ata agt ggg gct gcc act ttt tta	699
Ile Pro Lys Gly Lys Asp Tyr Ala Ile Ser Gly Ala Ala Thr Phe Leu	
175 180 185	
acc aac ttt ggg gat cga gaa acc gtg atg ggc gct tat cgt cat aat	747
Thr Asn Phe Gly Asp Arg Glu Thr Val Met Gly Ala Tyr Arg His Asn	
190 195 200 205	
cat ttt gat gcg ctt ttg tat tac acg cat caa aat att ttt tac tat	795
His Phe Asp Ala Leu Leu Tyr Tyr Thr His Gln Asn Ile Phe Tyr Tyr	
210 215 220	
cgt gat ggg gat aat gct aca aaa gat ctc ttt aga cct aaa gcg gag	843
Arg Asp Gly Asp Asn Ala Thr Lys Asp Leu Phe Arg Pro Lys Ala Glu	
225 230 235	
aat aaa gtt aca gaa gtc cta gcg agc aaa aca atg tgatgggctaa	889
Asn Lys Val Thr Glu Val Leu Ala Ser Lys Thr Met	
240 245	
gatcaatggg tattttgagcg aaagggatat tttaacgctc agttataaca tgaccagaga	949
caacgctaac	959

<210> 20

<211> 249

<212> PRT

<213> Helicobacter pylori

<400> 20

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			20					25					30		
Glu	Glu	Arg	Lys	Thr	Glu	Arg	Lys	Lys	Glu	Lys	Asn	Ala	Gln	His	Thr
		35					40				45				
Leu	Gly	Lys	Val	Thr	Thr	Gln	Ala	Ala	Lys	Ile	Phe	Asn	Tyr	Asn	Asn
	50					55					60				
Gln	Thr	Thr	Ile	Ser	Ser	Lys	Glu	Leu	Glu	Arg	Arg	Gln	Ala	Asn	Gln
65				70						75				80	
Ile	Ser	Asp	Met	Phe	Arg	Arg	Asn	Pro	Asn	Ile	Asn	Val	Gly	Gly	Gly
			85						90					95	
Ala	Val	Ile	Ala	Gln	Lys	Ile	Tyr	Val	Arg	Gly	Ile	Glu	Asp	Arg	Leu
			100					105					110		
Ala	Arg	Val	Thr	Val	Asp	Gly	Ala	Ala	Gln	Met	Gly	Ala	Ser	Tyr	Gly
		115				120						125			
His	Gln	Gly	Asn	Thr	Ile	Ile	Asp	Pro	Gly	Met	Leu	Lys	Ser	Val	Val
	130				135						140				
Val	Thr	Lys	Gly	Ala	Ala	Gln	Ala	Ser	Ala	Gly	Pro	Met	Ala	Leu	Ile
145				150						155				160	
Gly	Ala	Ile	Lys	Met	Glu	Thr	Lys	Ser	Ala	Ser	Asp	Phe	Ile	Pro	Lys
			165					170						175	
Gly	Lys	Asp	Tyr	Ala	Ile	Ser	Gly	Ala	Ala	Thr	Phe	Leu	Thr	Asn	Phe
		180					185					190			
Gly	Asp	Arg	Glu	Thr	Val	Met	Gly	Ala	Tyr	Arg	His	Asn	His	Phe	Asp
	195					200					205				
Ala	Leu	Leu	Tyr	Tyr	Thr	His	Gln	Asn	Ile	Phe	Tyr	Tyr	Arg	Asp	Gly
	210				215					220					
Asp	Asn	Ala	Thr	Lys	Asp	Leu	Phe	Arg	Pro	Lys	Ala	Glu	Asn	Lys	Val
225				230					235					240	
Thr	Glu	Val	Leu	Ala	Ser	Lys	Thr	Met							
			245												

<210> 21
 <211> 1397
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (138)...(1244)

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 tcatagcagg atcacc atg caa ttt caa aaa gcc tta tta cat tca tca 170
 Met Gln Phe Gln Lys Ala Leu Leu His Ser Ser
 1 5 10
 ttc ttt tta cct tta ttt tta tct ttt tgt atc gct gaa gaa aat ggg 218
 Phe Phe Leu Pro Leu Phe Leu Ser Phe Cys Ile Ala Glu Glu Asn Gly
 15 20 25
 gcg tat gcg agc gtg ggt ttt gaa tat tcc att agt cat gcc gtt gaa 266
 Ala Tyr Ala Ser Val Gly Phe Glu Tyr Ser Ile Ser His Ala Val Glu
 30 35 40

cac aat aac ccc ttt tta aat caa gaa cgc atc caa atc att tct aac	314
His Asn Asn Pro Phe Leu Asn Gln Glu Arg Ile Gln Ile Ile Ser Asn	
45 50 55	
gct caa aat aaa atc tat aaa ctc cat caa gtt aaa aat gaa atc aca	362
Ala Gln Asn Lys Ile Tyr Lys Leu His Gln Val Lys Asn Glu Ile Thr	
60 65 70 75	
agc atg cct aaa acc ttt gca tat atc aac aac gct tta aaa aac aac	410
Ser Met Pro Lys Thr Phe Ala Tyr Ile Asn Asn Ala Leu Lys Asn Asn	
80 85 90	
tcc aaa tta acc ccc act gaa atg caa gcc gaa caa tac tac ctc caa	458
Ser Lys Leu Thr Pro Thr Glu Met Gln Ala Glu Gln Tyr Tyr Leu Gln	
95 100 105	
tcc acc ttt caa aac att gaa aaa ata gta atg ctt agc ggt ggc gtt	506
Ser Thr Phe Gln Asn Ile Glu Lys Ile Val Met Leu Ser Gly Gly Val	
110 115 120	
tca tct aac cca caa tta gtc caa gcg ttg gaa aaa atg caa gaa ccc	554
Ser Ser Asn Pro Gln Leu Val Gln Ala Leu Glu Lys Met Gln Glu Pro	
125 130 135	
att act aac cct tta gaa ttt gaa gaa aac tta aga aat tta gaa gtg	602
Ile Thr Asn Pro Leu Glu Phe Glu Glu Asn Leu Arg Asn Leu Glu Val	
140 145 150 155	
caa ttt gct caa tct caa aac cgc atg ctt tct tct tta tct tct caa	650
Gln Phe Ala Gln Ser Gln Asn Arg Met Leu Ser Ser Leu Ser Ser Gln	
160 165 170	
atc gct gcc att tca aat tcc tta aac gcg ctt gat cct aac tct tat	698
Ile Ala Ala Ile Ser Asn Ser Leu Asn Ala Leu Asp Pro Asn Ser Tyr	
175 180 185	
tct aaa aac att tca agc atg tat ggg gtg agt ttg agc gta ggt tat	746
Ser Lys Asn Ile Ser Ser Met Tyr Gly Val Ser Leu Ser Val Gly Tyr	
190 195 200	
aag cat ttc ttt acc aag aaa aaa aat caa ggg ttg cgc tat tac ttg	794
Lys His Phe Phe Thr Lys Lys Lys Asn Gln Gly Leu Arg Tyr Tyr Leu	
205 210 215	
ttt tat gac tat ggt tac act aat ttt ggt ttt gtg ggc aat ggc ttt	842
Phe Tyr Asp Tyr Gly Tyr Thr Asn Phe Gly Phe Val Gly Asn Gly Phe	
220 225 230 235	
gat ggt tta ggc aaa atg aat aac cat ctc tat ggg ctt ggg ata gac	890
Asp Gly Leu Gly Lys Met Asn Asn His Leu Tyr Gly Leu Gly Ile Asp	
240 245 250	
tat ctt tat aat ttc att gat aat gca aaa aaa cac tct agc gta ggt	938
Tyr Leu Tyr Asn Phe Ile Asp Asn Ala Lys Lys His Ser Ser Val Gly	
255 260 265	
ttt tat ctg ggt ttt gct tta gcg ggg agt tcg tgg gta ggg agt ggt	986
Phe Tyr Leu Gly Phe Ala Leu Ala Gly Ser Ser Trp Val Gly Ser Gly	

270	275	280	
ttg agc atg tgg gtg agc	caa acg gat ttt atc aac aat tac ttg acg	1034	
Leu Ser Met Trp Val Ser	Gln Thr Asp Phe Ile Asn Asn Tyr Leu Thr		
285	290 295		
ggc tat caa gct aaa atg cac acg agt ttt ttc cag atc cct ttg aat	1082		
Gly Tyr Gln Ala Lys Met His Thr Ser Phe Phe Gln Ile Pro Leu Asn			
300	305 310 315		
ttt ggg gtt cgt gtg aat gtc aat agg cat aat ggc ttt gaa atg ggc	1130		
Phe Gly Val Arg Val Asn Val Asn Arg His Asn Gly Phe Glu Met Gly			
	320 325 330		
ttg aaa atc cct tta gcg atg aat tcc ttt tat gaa acg cat ggc aaa	1178		
Leu Lys Ile Pro Leu Ala Met Asn Ser Phe Tyr Glu Thr His Gly Lys			
	335 340 345		
ggg cta aac act tcc ctc ttt ttc aaa cgc ctt gtc atg ttt aac gtg	1226		
Gly Leu Asn Thr Ser Leu Phe Phe Lys Arg Leu Val Met Phe Asn Val			
	350 355 360		
agt tac gtt tat agt ttt taggggggta gaaataagca ccccttaaa	1274		
Ser Tyr Val Tyr Ser Phe			
365			
tgttatcgca acctttgaat tttaaaaact ctttagtttt tttgcctcaa atgatggacg	1334		
ctctcgcccc caagaccata attattagaa tcgacctcat ctataatgac cacaatagaa	1394		
gcc	1397		

<210> 22

<211> 369

<212> PRT

<213> Helicobacter pylori

<400> 22

Met Gln Phe Gln Lys Ala Leu Leu His Ser Ser Phe Phe Leu Pro Leu	
1 5 10 15	
Phe Leu Ser Phe Cys Ile Ala Glu Glu Asn Gly Ala Tyr Ala Ser Val	
20 25 30	
Gly Phe Glu Tyr Ser Ile Ser His Ala Val Glu His Asn Asn Pro Phe	
35 40 45	
Leu Asn Gln Glu Arg Ile Gln Ile Ile Ser Asn Ala Gln Asn Lys Ile	
50 55 60	
Tyr Lys Leu His Gln Val Lys Asn Glu Ile Thr Ser Met Pro Lys Thr	
65 70 75 80	
Phe Ala Tyr Ile Asn Asn Ala Leu Lys Asn Asn Ser Lys Leu Thr Pro	
85 90 95	
Thr Glu Met Gln Ala Glu Gln Tyr Tyr Leu Gln Ser Thr Phe Gln Asn	
100 105 110	
Ile Glu Lys Ile Val Met Leu Ser Gly Gly Val Ser Ser Asn Pro Gln	
115 120 125	
Leu Val Gln Ala Leu Glu Lys Met Gln Glu Pro Ile Thr Asn Pro Leu	
130 135 140	
Glu Phe Glu Glu Asn Leu Arg Asn Leu Glu Val Gln Phe Ala Gln Ser	
145 150 155 160	
Gln Asn Arg Met Leu Ser Ser Leu Ser Ser Gln Ile Ala Ala Ile Ser	
165 170 175	

Asn	Ser	Leu	Asn	Ala	Leu	Asp	Pro	Asn	Ser	Tyr	Ser	Lys	Asn	Ile	Ser
			180					185					190		
Ser	Met	Tyr	Gly	Val	Ser	Leu	Ser	Val	Gly	Tyr	Lys	His	Phe	Phe	Thr
		195					200					205			
Lys	Lys	Lys	Asn	Gln	Gly	Leu	Arg	Tyr	Tyr	Leu	Phe	Tyr	Asp	Tyr	Gly
		210				215					220				
Tyr	Thr	Asn	Phe	Gly	Phe	Val	Gly	Asn	Gly	Phe	Asp	Gly	Leu	Gly	Lys
225					230					235					240
Met	Asn	Asn	His	Leu	Tyr	Gly	Leu	Gly	Ile	Asp	Tyr	Leu	Tyr	Asn	Phe
			245						250					255	
Ile	Asp	Asn	Ala	Lys	Lys	His	Ser	Ser	Val	Gly	Phe	Tyr	Leu	Gly	Phe
		260						265					270		
Ala	Leu	Ala	Gly	Ser	Ser	Trp	Val	Gly	Ser	Gly	Leu	Ser	Met	Trp	Val
		275					280					285			
Ser	Gln	Thr	Asp	Phe	Ile	Asn	Asn	Tyr	Leu	Thr	Gly	Tyr	Gln	Ala	Lys
		290				295					300				
Met	His	Thr	Ser	Phe	Phe	Gln	Ile	Pro	Leu	Asn	Phe	Gly	Val	Arg	Val
305					310					315					320
Asn	Val	Asn	Arg	His	Asn	Gly	Phe	Glu	Met	Gly	Leu	Lys	Ile	Pro	Leu
			325						330					335	
Ala	Met	Asn	Ser	Phe	Tyr	Glu	Thr	His	Gly	Lys	Gly	Leu	Asn	Thr	Ser
		340						345					350		
Leu	Phe	Phe	Lys	Arg	Leu	Val	Met	Phe	Asn	Val	Ser	Tyr	Val	Tyr	Ser
		355					360					365			
Phe															

<210> 23
 <211> 1030
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (342)...(824)

<400> 23
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 agccttacaa aatatcttaa ataacgctaa aagcgcgcat tttaaatttg ttttagagag 120
 ccaaaacgcc gctcaatcta ttatagaaat tcaaagcctc ttgaaacaac tctccttaaa 180
 aaataatgaa atcttttttaa tgccttttagg cacaaataac aacgagctag acaaaaaatct 240
 aaaaacccta gcccccttag ccataaagca tggtttcagg ctaagcgata ggcttcatat 300
 ccgcttgtag gataatcaaa aagggtttta aaaagttaat c atg acc atc aaa gtt 356
 Met Thr Ile Lys Val
 1 5

ttt tcg ccc aaa tac ccc act gaa tta gaa gaa ttt tat gct gag cgt 404
 Phe Ser Pro Lys Tyr Pro Thr Glu Leu Glu Glu Phe Tyr Ala Glu Arg
 10 15 20

atc gct gac aac cct tta ggg ttt atc caa cgc ttg gat ctt ttg cct 452
 Ile Ala Asp Asn Pro Leu Gly Phe Ile Gln Arg Leu Asp Leu Leu Pro
 25 30 35

agt att agc ggg ttc gtt caa aaa ttg cgc gag cat ggc ggg gaa ttt 500
 Ser Ile Ser Gly Phe Val Gln Lys Leu Arg Glu His Gly Gly Glu Phe
 40 45 50

ttt gaa atg aga gag ggt aac aag ctc att ggg att tgt ggg ctt aat	548
Phe Glu Met Arg Glu Gly Asn Lys Leu Ile Gly Ile Cys Gly Leu Asn	
55 60 65	
cct atc aat caa aca gaa gcc gag ctg tgc aaa ttc cac ata aat agt	596
Pro Ile Asn Gln Thr Glu Ala Glu Leu Cys Lys Phe His Ile Asn Ser	
70 75 80 85	
gct tat caa tcc caa ggg cta ggt caa aaa ctc tat gag agc gtg gag	644
Ala Tyr Gln Ser Gln Gly Leu Gly Gln Lys Leu Tyr Glu Ser Val Glu	
90 95 100	
aaa tac gct ttc att aaa ggc tat act aaa atc tct ctg cat gtg agc	692
Lys Tyr Ala Phe Ile Lys Gly Tyr Thr Lys Ile Ser Leu His Val Ser	
105 110 115	
aaa agc caa atc aag gca tgc aac ctc tat caa aag ctg ggt ttt gtg	740
Lys Ser Gln Ile Lys Ala Cys Asn Leu Tyr Gln Lys Leu Gly Phe Val	
120 125 130	
cac atc aaa gaa gag gat tgc gtg gtg gag ttg ggc gaa gag act ttg	788
His Ile Lys Glu Glu Asp Cys Val Val Glu Leu Gly Glu Glu Thr Leu	
135 140 145	
att ttc ccc act ctt ttt atg gaa aag att ttg tct tgattggtgc	834
Ile Phe Pro Thr Leu Phe Met Glu Lys Ile Leu Ser	
150 155 160	
atccatttga cacacgcca agcgacattc aaactatcaa acttttcatta acacaaccca	894
attaacgcta aataaacctt aaaacaaaca ctcggttgta aaattttggt tttcaagcgc	954
ttcgcaaagt tttagaagcc ctatttaggg gttaacgcta aaataggcta tcaaaactac	1014
tttaatgatt ttatag	1030

<210> 24
 <211> 161
 <212> PRT
 <213> Helicobacter pylori

<400> 24
Met Thr Ile Lys Val Phe Ser Pro Lys Tyr Pro Thr Glu Leu Glu Glu
1 5 10 15
Phe Tyr Ala Glu Arg Ile Ala Asp Asn Pro Leu Gly Phe Ile Gln Arg
20 25 30
Leu Asp Leu Leu Pro Ser Ile Ser Gly Phe Val Gln Lys Leu Arg Glu
35 40 45
His Gly Gly Glu Phe Phe Glu Met Arg Glu Gly Asn Lys Leu Ile Gly
50 55 60
Ile Cys Gly Leu Asn Pro Ile Asn Gln Thr Glu Ala Glu Leu Cys Lys
65 70 75 80
Phe His Ile Asn Ser Ala Tyr Gln Ser Gln Gly Leu Gly Gln Lys Leu
85 90 95
Tyr Glu Ser Val Glu Lys Tyr Ala Phe Ile Lys Gly Tyr Thr Lys Ile
100 105 110
Ser Leu His Val Ser Lys Ser Gln Ile Lys Ala Cys Asn Leu Tyr Gln
115 120 125
Lys Leu Gly Phe Val His Ile Lys Glu Glu Asp Cys Val Val Glu Leu
130 135 140

Gly Glu Glu Thr Leu Ile Phe Pro Thr Leu Phe Met Glu Lys Ile Leu
 145 150 155 160
 Ser

<210> 25
 <211> 1477
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (374)...(1267)

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 caactaaaat ctctactaac aattcatctg aatgcaaaat ctcaattctc cctaaaaaac 120
 aaaatcactt ttaagactaa atcatgttag aattatactt gaatttacac tcagtttagt 180
 ttattttctta atacaaaagg taggcgtttt gaaacattta accccactca ctacacaccat 240
 ctttaaagcc ttatggctag gcacagcctt aagtgcactt ttaagtttag ccgcaacaga 300
 aagccccact aaaacagagc ctaagcccg ctaaaggggtt aaaaacaagc ccaaatcgcc 360
 cgttactaaa gtc atg atg acc aat tgc gac aat att aaa gat ttt aac 409
 Met Met Thr Asn Cys Asp Asn Ile Lys Asp Phe Asn
 1 5 10
 gct aag caa aaa gaa gtc tta aaa gcc gct tat caa ttc ggc tct aaa 457
 Ala Lys Gln Lys Glu Val Leu Lys Ala Ala Tyr Gln Phe Gly Ser Lys
 15 20 25
 gaa aat tta ggc tat gaa atg gca ggc att gca tgg aaa gag tca tgc 505
 Glu Asn Leu Gly Tyr Glu Met Ala Gly Ile Ala Trp Lys Glu Ser Cys
 30 35 40
 gca ggg gtt tat aaa atc aat ttt tgc gat ccg agc gcg ggc gtg tat 553
 Ala Gly Val Tyr Lys Ile Asn Phe Ser Asp Pro Ser Ala Gly Val Tyr
 45 50 55 60
 cat tct tat atc cca agc gtt cta aaa agc tat ggg cat aat gat agc 601
 His Ser Tyr Ile Pro Ser Val Leu Lys Ser Tyr Gly His Asn Asp Ser
 65 70 75
 ccc ttt ttg cgt aat gtg atg ggg gaa ttg ctc att aaa gac gat gcg 649
 Pro Phe Leu Arg Asn Val Met Gly Glu Leu Leu Ile Lys Asp Asp Ala
 80 85 90
 ttt gct tct gaa gtg gct tta aaa gag ttg ctc tat tgg aaa aca cgc 697
 Phe Ala Ser Glu Val Ala Leu Lys Glu Leu Leu Tyr Trp Lys Thr Arg
 95 100 105
 tac cat gac aat tta aaa gac atg att aaa tct tac aac aag ggc agt 745
 Tyr His Asp Asn Leu Lys Asp Met Ile Lys Ser Tyr Asn Lys Gly Ser
 110 115 120
 cgt tgg gaa agg agc gaa aaa tct aac gct gat gct gaa aaa tat tac 793
 Arg Trp Glu Arg Ser Glu Lys Ser Asn Ala Asp Ala Glu Lys Tyr Tyr
 125 130 135 140

gaa gag ata caa gac aga atc agg cgt ttg aaa gaa tct aaa atc ttt	841
Glu Glu Ile Gln Asp Arg Ile Arg Arg Leu Lys Glu Ser Lys Ile Phe	
145 150 155	
gat tcg cag tct agt aat gac caa gaa ttg caa aaa agc gct aat agc	889
Asp Ser Gln Ser Ser Asn Asp Gln Glu Leu Gln Lys Ser Ala Asn Ser	
160 165 170	
aac ctg gat tta gac cct atc ggc aac gcc atg ccc caa gcc tta att	937
Asn Leu Asp Leu Asp Pro Ile Gly Asn Ala Met Pro Gln Ala Leu Ile	
175 180 185	
gcc aaa gaa act aaa ata gaa gaa acc caa gca gaa aaa tcc caa gaa	985
Ala Lys Glu Thr Lys Ile Glu Glu Thr Gln Ala Glu Lys Ser Gln Glu	
190 195 200	
atg aaa gag aca act agc gag caa aca aaa agt aag cca gaa aaa gca	1033
Met Lys Glu Thr Thr Ser Glu Gln Thr Lys Ser Lys Pro Glu Lys Ala	
205 210 215 220	
aaa gat aaa ccc atg tat ttg gcg caa atc aac agc act gat ttc aca	1081
Lys Asp Lys Pro Met Tyr Leu Ala Gln Ile Asn Ser Thr Asp Phe Thr	
225 230 235	
ccc gtt aaa aaa agc ccc aaa aaa ccg gct aaa gtg agc caa aaa cac	1129
Pro Val Lys Lys Ser Pro Lys Lys Pro Ala Lys Val Ser Gln Lys His	
240 245 250	
tcc ttt aag aat aac att aaa aat aat gta aaa aac aac gcc aaa acc	1177
Ser Phe Lys Asn Asn Ile Lys Asn Asn Val Lys Asn Asn Ala Lys Thr	
255 260 265	
gct tcc aaa aaa caa gaa atg tgc aaa aat tgc tct cca ggg caa agg	1225
Ala Ser Lys Lys Gln Glu Met Cys Lys Asn Cys Ser Pro Gly Gln Arg	
270 275 280	
aat gcg att tta gct aac cac atc act ctc atg caa gag ctt	1267
Asn Ala Ile Leu Ala Asn His Ile Thr Leu Met Gln Glu Leu	
285 290 295	
taaaaagtcc taaaaatggc gcaaaaaact cttttgatta tcactgatgg cattgggtat	1327
cgtaaagata gcgatcataa cgctttcttc catgccaaaa aaccactta tgatttgatg	1387
tttaaaacct tgccttatag cctgattgat acgcatggct tgagcgtggg cttacctaa	1447
gggcaaatgg gaaattctga agtggggcat	1477

<210> 26

<211> 298

<212> PRT

<213> *Helicobacter pylori*

<400> 26

Met Met Thr Asn Cys Asp Asn Ile Lys Asp Phe Asn Ala Lys Gln Lys	
1 5 10 15	
Glu Val Leu Lys Ala Ala Tyr Gln Phe Gly Ser Lys Glu Asn Leu Gly	
20 25 30	
Tyr Glu Met Ala Gly Ile Ala Trp Lys Glu Ser Cys Ala Gly Val Tyr	
35 40 45	
Lys Ile Asn Phe Ser Asp Pro Ser Ala Gly Val Tyr His Ser Tyr Ile	

50	55	60
Pro Ser Val Leu Lys	Ser Tyr Gly His Asn Asp	Ser Pro Phe Leu Arg
65	70	75
Asn Val Met Gly Glu	Leu Leu Ile Lys Asp	Ala Phe Ala Ser Glu
	85	90
Val Ala Leu Lys Glu	Leu Leu Tyr Trp Lys	Thr Arg Tyr His Asp Asn
	100	105
Leu Lys Asp Met Ile	Lys Ser Tyr Asn Lys	Gly Ser Arg Trp Glu Arg
	115	120
Ser Glu Lys Ser Asn	Ala Asp Ala Glu Lys	Tyr Tyr Glu Glu Ile Gln
	130	135
Asp Arg Ile Arg Arg	Leu Lys Glu Ser Lys	Ile Phe Asp Ser Gln Ser
	145	150
Ser Asn Asp Gln Glu	Leu Gln Lys Ser Ala	Asn Ser Asn Leu Asp Leu
	165	170
Asp Pro Ile Gly Asn	Ala Met Pro Gln Ala	Leu Ile Ala Lys Glu Thr
	180	185
Lys Ile Glu Glu Thr	Gln Ala Glu Lys Ser	Gln Glu Met Lys Glu Thr
	195	200
Thr Ser Glu Gln Thr	Lys Ser Lys Pro Glu	Lys Ala Lys Asp Lys Pro
	210	215
Met Tyr Leu Ala Gln	Ile Asn Ser Thr Asp	Phe Thr Pro Val Lys Lys
	225	230
Ser Pro Lys Lys Pro	Ala Lys Val Ser Gln	Lys His Ser Phe Lys Asn
	245	250
Asn Ile Lys Asn Asn	Val Lys Asn Asn Ala	Lys Thr Ala Ser Lys Lys
	260	265
Gln Glu Met Cys Lys	Asn Cys Ser Pro Gly	Gln Arg Asn Ala Ile Leu
	275	280
Ala Asn His Ile Thr	Leu Met Gln Glu Leu	
	290	295

<210> 27
 <211> 1515
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (141)...(1340)

<400> 27
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 atgggggttg atttgattta tggcatcatt cgggtggctct ttttaatggg aaaaattatt 120
 ttttaataaaa ataaaagcgc atg aaa gaa tct ttt tac ata gag gga atg act 173
 Met Lys Glu Ser Phe Tyr Ile Glu Gly Met Thr
 1 5 10

tgc acg gcg tgt tct agc ggg att gaa cgc tct ttg ggg cgt aag agt 221
 Cys Thr Ala Cys Ser Ser Gly Ile Glu Arg Ser Leu Gly Arg Lys Ser
 15 20 25

ttt gtg aaa aaa ata gaa gtg agc ctt tta aat aag agc gct aac att 269
 Phe Val Lys Lys Ile Glu Val Ser Leu Leu Asn Lys Ser Ala Asn Ile
 30 35 40

gaa ttt gac gaa aac caa acc aat tta gac gaa att ttt aaa ctc att 317

Glu	Phe	Asp	Glu	Asn	Gln	Thr	Asn	Leu	Asp	Glu	Ile	Phe	Lys	Leu	Ile		
45						50					55						
gaa	aag	cta	ggc	tat	agc	cct	aaa	aaa	gct	ctg	aca	aaa	gaa	aaa	aaa	365	
Glu	Lys	Leu	Gly	Tyr	Ser	Pro	Lys	Lys	Ala	Leu	Thr	Lys	Glu	Lys	Lys		
60					65				70						75		
gaa	ttt	ttt	agc	cct	aat	gtt	aaa	tta	gcg	tta	gcg	gtt	att	ttc	acg	413	
Glu	Phe	Phe	Ser	Pro	Asn	Val	Lys	Leu	Ala	Leu	Ala	Val	Ile	Phe	Thr		
			80						85					90			
ctt	ttt	gtg	gtg	tat	ctt	tct	atg	ggg	gcg	atg	ctt	agc	cct	agc	ctt	461	
Leu	Phe	Val	Val	Tyr	Leu	Ser	Met	Gly	Ala	Met	Leu	Ser	Pro	Ser	Leu		
			95					100					105				
tta	cct	gaa	agc	ttg	ctt	gca	att	gat	aat	cat	agt	aat	ttt	tta	aac	509	
Leu	Pro	Glu	Ser	Leu	Leu	Ala	Ile	Asp	Asn	His	Ser	Asn	Phe	Leu	Asn		
		110					115					120					
gct	tgc	tta	cag	ctt	ata	ggc	gca	ctc	att	gtc	atg	cat	ttg	ggg	agg	557	
Ala	Cys	Leu	Gln	Leu	Ile	Gly	Ala	Leu	Ile	Val	Met	His	Leu	Gly	Arg		
		125				130				135							
gat	ttt	tac	att	caa	ggg	ttt	aaa	gcc	tta	tgg	cac	aga	caa	ccc	aac	605	
Asp	Phe	Tyr	Ile	Gln	Gly	Phe	Lys	Ala	Leu	Trp	His	Arg	Gln	Pro	Asn		
140					145					150					155		
atg	agc	agc	ctt	atc	gcc	ata	ggc	aca	agc	gct	gcc	tta	att	tca	agc	653	
Met	Ser	Ser	Leu	Ile	Ala	Ile	Gly	Thr	Ser	Ala	Ala	Leu	Ile	Ser	Ser		
				160					165					170			
ctg	tgg	caa	ttg	tat	ttg	gtc	tat	acc	aat	cat	tat	acc	gat	cag	tgg	701	
Leu	Trp	Gln	Leu	Tyr	Leu	Val	Tyr	Thr	Asn	His	Tyr	Thr	Asp	Gln	Trp		
			175					180					185				
tct	tat	ggg	cat	tat	tat	ttt	gaa	agc	gtg	tgc	gtg	att	tta	atg	ttt	749	
Ser	Tyr	Gly	His	Tyr	Tyr	Phe	Glu	Ser	Val	Cys	Val	Ile	Leu	Met	Phe		
		190					195					200					
gtg	atg	gtg	ggc	aaa	cgc	att	gaa	aat	gtt	tct	aaa	gac	aaa	gct	tta	797	
Val	Met	Val	Gly	Lys	Arg	Ile	Glu	Asn	Val	Ser	Lys	Asp	Lys	Ala	Leu		
		205				210					215						
gac	gct	atg	caa	gcc	ttg	atg	aaa	aac	gcc	cca	aaa	acc	gcc	ctt	aaa	845	
Asp	Ala	Met	Gln	Ala	Leu	Met	Lys	Asn	Ala	Pro	Lys	Thr	Ala	Leu	Lys		
				225					230					235			
atg	caa	aat	aac	caa	cag	att	gaa	gtt	tta	gtg	gat	agc	att	gtg	gtg	893	
Met	Gln	Asn	Asn	Gln	Gln	Ile	Glu	Val	Leu	Val	Asp	Ser	Ile	Val	Val		
				240					245					250			
ggg	gat	att	cta	aaa	gtc	ctc	cct	gga	agc	gcg	att	gcg	gtg	gat	ggt	941	
Gly	Asp	Ile	Leu	Lys	Val	Leu	Pro	Gly	Ser	Ala	Ile	Ala	Val	Asp	Gly		
			255					260					265				
gaa	atc	ata	gag	ggc	gaa	ggg	gaa	tta	gat	gag	agc	atg	ttg	agc	ggc	989	
Glu	Ile	Ile	Glu	Gly	Glu	Gly	Glu	Leu	Asp	Glu	Ser	Met	Leu	Ser	Gly		
		270					275					280					

gaa gcg ttg ccg gtt tat aaa aaa gtc ggc gat aaa gtc ttt tca ggg 1037
 Glu Ala Leu Pro Val Tyr Lys Lys Val Gly Asp Lys Val Phe Ser Gly
 285 290 295

 aca ttc aat agc cac acg agt ttt tta atg aaa gcc acg caa aac aac 1085
 Thr Phe Asn Ser His Thr Ser Phe Leu Met Lys Ala Thr Gln Asn Asn
 300 305 310 315

 aaa aac agc acc ttg tct caa att ata gaa atg att tat aac gct caa 1133
 Lys Asn Ser Thr Leu Ser Gln Ile Ile Glu Met Ile Tyr Asn Ala Gln
 320 325 330

 agt tca aag gca gag att tct cgc tta gcg gat aag gtt tca agc gtg 1181
 Ser Ser Lys Ala Glu Ile Ser Arg Leu Ala Asp Lys Val Ser Ser Val
 335 340 345

 ttt gtg cca agc gtg atc gct att tct att tta gcg ttt gtg gtg tgg 1229
 Phe Val Pro Ser Val Ile Ala Ile Ser Ile Leu Ala Phe Val Val Trp
 350 355 360

 ctc atc att gca cct aag ccc gat ttt tgg tgg aat ttt gga atc gct 1277
 Leu Ile Ile Ala Pro Lys Pro Asp Phe Trp Trp Asn Phe Gly Ile Ala
 365 370 375

 tta gaa gtg ttt gta tcg gtt tta gtg att tct tgc cct tgc gct tta 1325
 Leu Glu Val Phe Val Ser Val Leu Val Ile Ser Cys Pro Cys Ala Leu
 380 385 390 395

 gga ttg cta cgc cta tgagcatttt agtagcgaac cagaaagcga gttcttttagg 1380
 Gly Leu Leu Arg Leu
 400

 gttatttttt aaagacgcta aaagttttaga aaaagcaagg ctagtcaata cgatcgtttt 1440
 tgataaaacc ggcacgctca ctaacggcaa gcctgtcggtt aaaagcgttc attctaagat 1500
 agaattatta gagtt 1515

<210> 28
 <211> 400
 <212> PRT
 <213> Helicobacter pylori

<400> 28
 Met Lys Glu Ser Phe Tyr Ile Glu Gly Met Thr Cys Thr Ala Cys Ser
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 Ser Gly Ile Glu Arg Ser Leu Gly Arg Lys Ser Phe Val Lys Lys Ile
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 Glu Val Ser Leu Leu Asn Lys Ser Ala Asn Ile Glu Phe Asp Glu Asn
 35 40 45
 Gln Thr Asn Leu Asp Glu Ile Phe Lys Leu Ile Glu Lys Leu Gly Tyr
 50 55 60
 Ser Pro Lys Lys Ala Leu Thr Lys Glu Lys Lys Glu Phe Phe Ser Pro
 65 70 75 80
 Asn Val Lys Leu Ala Leu Ala Val Ile Phe Thr Leu Phe Val Val Tyr
 85 90 95
 Leu Ser Met Gly Ala Met Leu Ser Pro Ser Leu Leu Pro Glu Ser Leu
 100 105 110
 Leu Ala Ile Asp Asn His Ser Asn Phe Leu Asn Ala Cys Leu Gln Leu

115	120	125
Ile Gly Ala Leu Ile Val Met His Leu Gly Arg Asp Phe Tyr Ile Gln		
130	135	140
Gly Phe Lys Ala Leu Trp His Arg Gln Pro Asn Met Ser Ser Leu Ile		
145	150	155
Ala Ile Gly Thr Ser Ala Ala Leu Ile Ser Ser Leu Trp Gln Leu Tyr		
165	170	175
Leu Val Tyr Thr Asn His Tyr Thr Asp Gln Trp Ser Tyr Gly His Tyr		
180	185	190
Tyr Phe Glu Ser Val Cys Val Ile Leu Met Phe Val Met Val Gly Lys		
195	200	205
Arg Ile Glu Asn Val Ser Lys Asp Lys Ala Leu Asp Ala Met Gln Ala		
210	215	220
Leu Met Lys Asn Ala Pro Lys Thr Ala Leu Lys Met Gln Asn Asn Gln		
225	230	235
Gln Ile Glu Val Leu Val Asp Ser Ile Val Val Gly Asp Ile Leu Lys		
245	250	255
Val Leu Pro Gly Ser Ala Ile Ala Val Asp Gly Glu Ile Ile Glu Gly		
260	265	270
Glu Gly Glu Leu Asp Glu Ser Met Leu Ser Gly Glu Ala Leu Pro Val		
275	280	285
Tyr Lys Lys Val Gly Asp Lys Val Phe Ser Gly Thr Phe Asn Ser His		
290	295	300
Thr Ser Phe Leu Met Lys Ala Thr Gln Asn Asn Lys Asn Ser Thr Leu		
305	310	315
Ser Gln Ile Ile Glu Met Ile Tyr Asn Ala Gln Ser Ser Lys Ala Glu		
325	330	335
Ile Ser Arg Leu Ala Asp Lys Val Ser Ser Val Phe Val Pro Ser Val		
340	345	350
Ile Ala Ile Ser Ile Leu Ala Phe Val Val Trp Leu Ile Ile Ala Pro		
355	360	365
Lys Pro Asp Phe Trp Trp Asn Phe Gly Ile Ala Leu Glu Val Phe Val		
370	375	380
Ser Val Leu Val Ile Ser Cys Pro Cys Ala Leu Gly Leu Leu Arg Leu		
385	390	395
		400

<210> 29
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 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (76)...(1389)

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 tagtagagag atggg atg aaa aaa ata tgg ctt tta gtg tgg ggc ttg tgt 111
 Met Lys Lys Ile Trp Leu Leu Val Trp Gly Leu Cys
 1 5 10

 tct tgg gtg ttt ttg cat gcg ata gag atg ata gaa aaa gcc cct aca 159
 Ser Trp Val Phe Leu His Ala Ile Glu Met Ile Glu Lys Ala Pro Thr
 15 20 25

 aat gta gag gat aga gac aaa gcc ccc cat ttg ttg ctt tta gca ggg 207
 Asn Val Glu Asp Arg Asp Lys Ala Pro His Leu Leu Leu Leu Ala Gly

30	35	40	
att caa ggc gat gag cct ggt ggg ttt aat gca act aat ttg ttt tta Ile Gln Gly Asp Glu Pro Gly Gly Phe Asn Ala Thr Asn Leu Phe Leu 45 50 55 60			255
atg cat tat agc gtt tta aaa ggt ttg gtt gaa gtg gtt cct gta ttg Met His Tyr Ser Val Leu Lys Gly Leu Val Glu Val Val Pro Val Leu 65 70 75			303
aat aag cct tcc atg tta aga aat cat agg ggc ttg tat ggg gat atg Asn Lys Pro Ser Met Leu Arg Asn His Arg Gly Leu Tyr Gly Asp Met 80 85 90			351
aac cgc aaa ttt gcc gct tta gac aag aat gac cct gaa tac ccc act Asn Arg Lys Phe Ala Ala Leu Asp Lys Asn Asp Pro Glu Tyr Pro Thr 95 100 105			399
atc cag gaa atc aaa tcc ttg att gca aaa ccc agt ata gac gct gtc Ile Gln Glu Ile Lys Ser Leu Ile Ala Lys Pro Ser Ile Asp Ala Val 110 115 120			447
ttg cat ttg cat gat ggc ggt ggg tat tac cgc cct gtt tat gtt gat Leu His Leu His Asp Gly Gly Tyr Tyr Arg Pro Val Tyr Val Asp 125 130 135 140			495
gcg atg ctc aat cct aag cgc tgg ggg aat tgc ttt att att gat caa Ala Met Leu Asn Pro Lys Arg Trp Gly Asn Cys Phe Ile Ile Asp Gln 145 150 155			543
gat gag gtt aaa ggg gcg aaa ttc cct aat ttg ctt gct ttt gca aac Asp Glu Val Lys Gly Ala Lys Phe Pro Asn Leu Leu Ala Phe Ala Asn 160 165 170			591
aat acg att gag agt atc aac gcc cat tta ttg cac ccc att gaa gag Asn Thr Ile Glu Ser Ile Asn Ala His Leu Leu His Pro Ile Glu Glu 175 180 185			639
tat cat tta aaa aac acg cgc acc gcg caa ggc gat aca gaa atg caa Tyr His Leu Lys Asn Thr Arg Thr Ala Gln Gly Asp Thr Glu Met Gln 190 195 200			687
aaa gcc cta act ttt tat gcg atc aac caa aaa aag agc gct ttt gcc Lys Ala Leu Thr Phe Tyr Ala Ile Asn Gln Lys Lys Ser Ala Phe Ala 205 210 215 220			735
aat gaa gct agc aaa gaa ctc cct tta gca tca agg gtg ttt tac cac Asn Glu Ala Ser Lys Glu Leu Pro Leu Ala Ser Arg Val Phe Tyr His 225 230 235			783
ctg caa gcc att gag ggc tta ctc aat cag ctc aat atc cct ttt aag Leu Gln Ala Ile Glu Gly Leu Leu Asn Gln Leu Asn Ile Pro Phe Lys 240 245 250			831
cgc gat ttt gat ctt aac cct aac agc gtg cat gcc cta atc aat gat Arg Asp Phe Asp Leu Asn Pro Asn Ser Val His Ala Leu Ile Asn Asp 255 260 265			879

aaa aac ttg tgg gca aaa atc agc tct ttg cct aaa atg ccc ctt ttt	927
Lys Asn Leu Trp Ala Lys Ile Ser Ser Leu Pro Lys Met Pro Leu Phe	
270 275 280	
aac ttg cgc cct aaa ctc aat cat ttc ccc tta ccc cac aac act aaa	975
Asn Leu Arg Pro Lys Leu Asn His Phe Pro Leu Pro His Asn Thr Lys	
285 290 295 300	
atc cca caa atc ccc ata gag agc aac gct tac att gta ggg cta gtc	1023
Ile Pro Gln Ile Pro Ile Glu Ser Asn Ala Tyr Ile Val Gly Leu Val	
305 310 315	
aaa aat aaa caa gaa gtg ttt tta aaa tac ggc aac aag ctc atg aca	1071
Lys Asn Lys Gln Glu Val Phe Leu Lys Tyr Gly Asn Lys Leu Met Thr	
320 325 330	
cga tta tcg cct ttt tac ata gag ttt gat cct tct tta gaa gaa gtg	1119
Arg Leu Ser Pro Phe Tyr Ile Glu Phe Asp Pro Ser Leu Glu Glu Val	
335 340 345	
aaa atg caa att gac aat aag gat caa atg gtt aaa ata ggg agc gtg	1167
Lys Met Gln Ile Asp Asn Lys Asp Gln Met Val Lys Ile Gly Ser Val	
350 355 360	
gtt gaa gtg aaa gag agt ttt tat atc cat gct atg gac aat atc cgt	1215
Val Glu Val Lys Glu Ser Phe Tyr Ile His Ala Met Asp Asn Ile Arg	
365 370 375 380	
gcg aat gtg att ggc ttt agc gtt tct aat gaa aat aag cct aat gaa	1263
Ala Asn Val Ile Gly Phe Ser Val Ser Asn Glu Asn Lys Pro Asn Glu	
385 390 395	
gcg ggt tat acg att aaa ttt aaa gat ttt caa aaa cgc ttt tca ttg	1311
Ala Gly Tyr Thr Ile Lys Phe Lys Asp Phe Gln Lys Arg Phe Ser Leu	
400 405 410	
gac aag caa gaa agg atc tat cgc ata gaa ttt tat aaa aac aac gcg	1359
Asp Lys Gln Glu Arg Ile Tyr Arg Ile Glu Phe Tyr Lys Asn Asn Ala	
415 420 425	
ttt agc ggg atg atc tta gtg aaa ttt gtg taggaatgga taaatctcat	1409
Phe Ser Gly Met Ile Leu Val Lys Phe Val	
430 435	

tgcccttttaa cattcaaggg ttttggtatt tttt 1443

<210> 30

<211> 438

<212> PRT

<213> *Helicobacter pylori*

<400> 30

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Leu His Ala Ile Glu Met Ile Glu Lys Ala Pro Thr Asn Val Glu Asp	
20 25 30	
Arg Asp Lys Ala Pro His Leu Leu Leu Ala Gly Ile Gln Gly Asp	
35 40 45	

Glu	Pro	Gly	Gly	Phe	Asn	Ala	Thr	Asn	Leu	Phe	Leu	Met	His	Tyr	Ser
50						55					60				
Val	Leu	Lys	Gly	Leu	Val	Glu	Val	Val	Pro	Val	Leu	Asn	Lys	Pro	Ser
65					70					75					80
Met	Leu	Arg	Asn	His	Arg	Gly	Leu	Tyr	Gly	Asp	Met	Asn	Arg	Lys	Phe
			85						90					95	
Ala	Ala	Leu	Asp	Lys	Asn	Asp	Pro	Glu	Tyr	Pro	Thr	Ile	Gln	Glu	Ile
			100					105					110		
Lys	Ser	Leu	Ile	Ala	Lys	Pro	Ser	Ile	Asp	Ala	Val	Leu	His	Leu	His
			115				120						125		
Asp	Gly	Gly	Gly	Tyr	Tyr	Arg	Pro	Val	Tyr	Val	Asp	Ala	Met	Leu	Asn
			130			135					140				
Pro	Lys	Arg	Trp	Gly	Asn	Cys	Phe	Ile	Ile	Asp	Gln	Asp	Glu	Val	Lys
145					150					155					160
Gly	Ala	Lys	Phe	Pro	Asn	Leu	Leu	Ala	Phe	Ala	Asn	Asn	Thr	Ile	Glu
			165						170					175	
Ser	Ile	Asn	Ala	His	Leu	Leu	His	Pro	Ile	Glu	Glu	Tyr	His	Leu	Lys
			180					185					190		
Asn	Thr	Arg	Thr	Ala	Gln	Gly	Asp	Thr	Glu	Met	Gln	Lys	Ala	Leu	Thr
			195				200						205		
Phe	Tyr	Ala	Ile	Asn	Gln	Lys	Lys	Ser	Ala	Phe	Ala	Asn	Glu	Ala	Ser
			210			215						220			
Lys	Glu	Leu	Pro	Leu	Ala	Ser	Arg	Val	Phe	Tyr	His	Leu	Gln	Ala	Ile
225					230					235					240
Glu	Gly	Leu	Leu	Asn	Gln	Leu	Asn	Ile	Pro	Phe	Lys	Arg	Asp	Phe	Asp
				245					250					255	
Leu	Asn	Pro	Asn	Ser	Val	His	Ala	Leu	Ile	Asn	Asp	Lys	Asn	Leu	Trp
			260					265					270		
Ala	Lys	Ile	Ser	Ser	Leu	Pro	Lys	Met	Pro	Leu	Phe	Asn	Leu	Arg	Pro
			275				280						285		
Lys	Leu	Asn	His	Phe	Pro	Leu	Pro	His	Asn	Thr	Lys	Ile	Pro	Gln	Ile
			290			295					300				
Pro	Ile	Glu	Ser	Asn	Ala	Tyr	Ile	Val	Gly	Leu	Val	Lys	Asn	Lys	Gln
305				310						315					320
Glu	Val	Phe	Leu	Lys	Tyr	Gly	Asn	Lys	Leu	Met	Thr	Arg	Leu	Ser	Pro
				325					330					335	
Phe	Tyr	Ile	Glu	Phe	Asp	Pro	Ser	Leu	Glu	Glu	Val	Lys	Met	Gln	Ile
			340					345					350		
Asp	Asn	Lys	Asp	Gln	Met	Val	Lys	Ile	Gly	Ser	Val	Val	Glu	Val	Lys
			355				360					365			
Glu	Ser	Phe	Tyr	Ile	His	Ala	Met	Asp	Asn	Ile	Arg	Ala	Asn	Val	Ile
			370			375					380				
Gly	Phe	Ser	Val	Ser	Asn	Glu	Asn	Lys	Pro	Asn	Glu	Ala	Gly	Tyr	Thr
385					390					395					400
Ile	Lys	Phe	Lys	Asp	Phe	Gln	Lys	Arg	Phe	Ser	Leu	Asp	Lys	Gln	Glu
				405					410					415	
Arg	Ile	Tyr	Arg	Ile	Glu	Phe	Tyr	Lys	Asn	Asn	Ala	Phe	Ser	Gly	Met
			420					425					430		
Ile	Leu	Val	Lys	Phe	Val										
			435												

<210> 31

<211> 1280

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS
 <222> (66)...(1223)

<400> 31

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 ttcaa atg tta agg aaa aac att tta gct tac tat ggg gcg aat ttt ctc 110
 Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe Leu
 1 5 10 15

tta atc atc gct caa agc tta ccc cat gcg att tta acc ccc ttg ttg 158
 Leu Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu Leu
 20 25 30

ctt tct aaa ggg ctt agt ttg agt gaa atc ttg ctc gtg caa acc ttt 206
 Leu Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr Phe
 35 40 45

ttt agc ttt tgc gtg cta gtg gct gaa tac cca agc ggc gtt tta gcg 254
 Phe Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu Ala
 50 55 60

gat ttg atg agc cga aaa aat tta ttc ctg gtt tct aat gcc ttt tta 302
 Asp Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Ala Phe Leu
 65 70 75

atc gct agt ttt tcg ttt gtg ctg ttt ttt gat agc ttt att ttc atg 350
 Ile Ala Ser Phe Ser Phe Val Leu Phe Phe Asp Ser Phe Ile Phe Met
 80 85 90 95

ctt tta gcg tgg ggg ttg tat ggt ttg tat agc gca tgc tct agc ggc 398
 Leu Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser Gly
 100 105 110

acg att gaa gct tca ctc atc aca gac att aag gaa aac aaa aaa gat 446
 Thr Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys Asp
 115 120 125

tta tcc aag ttt tta gcc aaa aac aat caa att act tat tta ggc atg 494
 Leu Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly Met
 130 135 140

att ata ggg agt tct ttg gga tcg ttt ttg tat ctc aaa gtc cat gcg 542
 Ile Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His Ala
 145 150 155

atg ctg tat att gtg ggg att ttt tta atc atg ctc tgt gtg cta acg 590
 Met Leu Tyr Ile Val Gly Ile Phe Leu Ile Met Leu Cys Val Leu Thr
 160 165 170 175

atc att ttt tat ttt aaa gag aaa gaa ggg gat ttt aaa agc caa aaa 638
 Ile Ile Phe Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln Lys
 180 185 190

agc ctg aaa ctc ctt aaa gag caa gtc aaa ggc agt ctt aaa gag ctt 686
 Ser Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu Leu
 195 200 205

aaa gat aac ccc aaa ctt aaa att ctg tta gtg ggg cat ttg att acg 734

Lys	Asp	Asn	Pro	Lys	Leu	Lys	Ile	Leu	Leu	Val	Gly	His	Leu	Ile	Thr	
		210					215					220				
ccc	gtc	ttt	ttt	atg	agc	cat	ttt	caa	atg	tgg	caa	gcg	tat	ttt	tta	782
Pro	Val	Phe	Phe	Met	Ser	His	Phe	Gln	Met	Trp	Gln	Ala	Tyr	Phe	Leu	
	225					230					235					
aaa	caa	ggc	gtt	aaa	gag	caa	tac	ctt	ttt	gtg	ttt	tat	atc	gct	ttt	830
Lys	Gln	Gly	Val	Lys	Glu	Gln	Tyr	Leu	Phe	Val	Phe	Tyr	Ile	Ala	Phe	
	240				245					250					255	
caa	gtg	att	tct	att	ctc	att	cat	ttt	tta	aaa	gcc	tct	agt	tat	agc	878
Gln	Val	Ile	Ser	Ile	Leu	Ile	His	Phe	Leu	Lys	Ala	Ser	Ser	Tyr	Ser	
				260					265						270	
caa	aaa	atc	gcc	ttg	agt	tcg	ctt	gtg	gtg	ttg	tta	ggc	gtt	agc	ccc	926
Gln	Lys	Ile	Ala	Leu	Ser	Ser	Leu	Val	Val	Leu	Leu	Gly	Val	Ser	Pro	
			275					280					285			
tta	ttg	ctt	agc	aat	atc	cct	tat	tgt	ttc	ata	ggg	gtg	tat	gcg	ctc	974
Leu	Leu	Leu	Ser	Asn	Ile	Pro	Tyr	Cys	Phe	Ile	Gly	Val	Tyr	Ala	Leu	
		290				295						300				
atg	gtg	gcg	ttt	ttc	act	tac	atg	agc	tat	tgc	tta	aac	tat	caa	ttc	1022
Met	Val	Ala	Phe	Phe	Thr	Tyr	Met	Ser	Tyr	Cys	Leu	Asn	Tyr	Gln	Phe	
	305					310					315					
tcc	aaa	ttc	gtt	tct	aaa	aac	aac	att	tcc	tcg	ctc	tca	tcg	ctt	tta	1070
Ser	Lys	Phe	Val	Ser	Lys	Asn	Asn	Ile	Ser	Ser	Leu	Ser	Ser	Leu	Leu	
	320				325				330						335	
tca	agc	tgt	gtg	cgc	gtg	gtc	tct	gtg	cta	atc	tta	tcg	ctc	agc	agt	1118
Ser	Ser	Cys	Val	Arg	Val	Val	Ser	Val	Leu	Ile	Leu	Ser	Leu	Ser	Ser	
				340					345					350		
ctg	gaa	ctg	cgt	tac	ttc	tca	ccc	cta	act	atc	ata	acc	atg	cat	ttt	1166
Leu	Glu	Leu	Arg	Tyr	Phe	Ser	Pro	Leu	Thr	Ile	Ile	Thr	Met	His	Phe	
			355					360					365			
gcc	ttg	acg	ctt	atc	atc	ctc	ttt	ttc	ttt	ttg	tat	aag	gct	aag	ccg	1214
Ala	Leu	Thr	Leu	Ile	Ile	Leu	Phe	Phe	Phe	Leu	Tyr	Lys	Ala	Lys	Pro	
		370				375						380				
ttt	gat	gag	tgagcggcctt	taagagtgc	accttttagc	gatttctata										1263
Phe	Asp	Glu														
		385														
gcaacatcat	agccatg															1280
<210>	32															
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<212>	PRT															
<213>	Helicobacter pylori															
<400>	32															
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1				5					10				15			
Ile	Ile	Ala	Gln	Ser	Leu	Pro	His	Ala	Ile	Leu	Thr	Pro	Leu	Leu	Leu	

<400> 33

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							Met	Glu								
							1									
tca	gta	aaa	aca	gga	aaa	aca	aat	aag	ggt	ggc	aag	aat	aca	gag	atg	104
Ser	Val	Lys	Thr	Gly	Lys	Thr	Asn	Lys	Val	Gly	Lys	Asn	Thr	Glu	Met	
		5					10					15				
gct	aat	aca	aag	gca	aat	aaa	gag	gct	cat	ttt	aaa	caa	gcg	agc	acc	152
Ala	Asn	Thr	Lys	Ala	Asn	Lys	Glu	Ala	His	Phe	Lys	Gln	Ala	Ser	Thr	
	20					25					30					
att	aca	aat	ata	atc	aga	tca	att	cgt	ggg	att	ttt	aca	aaa	att	gca	200
Ile	Thr	Asn	Ile	Ile	Arg	Ser	Ile	Arg	Gly	Ile	Phe	Thr	Lys	Ile	Ala	
	35				40					45					50	
aag	aaa	ggt	aga	gga	ctt	gta	aaa	aaa	cac	ccc	aag	aaa	agc	agt	gcg	248
Lys	Lys	Val	Arg	Gly	Leu	Val	Lys	Lys	His	Pro	Lys	Lys	Ser	Ser	Ala	
				55					60					65		
gca	tta	gta	gta	ttg	acc	cat	att	gcg	tgc	aag	aaa	gcg	aaa	gaa	tta	296
Ala	Leu	Val	Val	Leu	Thr	His	Ile	Ala	Cys	Lys	Lys	Ala	Lys	Glu	Leu	
			70					75					80			
gac	gat	aaa	gtc	caa	gat	aaa	tcc	aaa	caa	gct	gaa	aaa	gaa	aat	caa	344
Asp	Asp	Lys	Val	Gln	Asp	Lys	Ser	Lys	Gln	Ala	Glu	Lys	Glu	Asn	Gln	
		85					90					95				
atc	aat	tggt	tggt	aaa	tat	tca	gga	tta	aca	ata	gcg	aca	agt	tta	tta	392
Ile	Asn	Trp	Trp	Lys	Tyr	Ser	Gly	Leu	Thr	Ile	Ala	Thr	Ser	Leu	Leu	
	100					105					110					
tta	gcc	gct	tgt	agc	act	ggt	gat	ggt	agt	gaa	caa	ata	gaa	cta	gaa	440
Leu	Ala	Ala	Cys	Ser	Thr	Gly	Asp	Val	Ser	Glu	Gln	Ile	Glu	Leu	Glu	
	115				120					125					130	
caa	gaa	aaa	caa	aag	acg	agc	aat	ata	gag	act	aac	aat	caa	ata	aaa	488
Gln	Glu	Lys	Gln	Lys	Thr	Ser	Asn	Ile	Glu	Thr	Asn	Asn	Gln	Ile	Lys	
				135					140					145		
gta	gaa	caa	gaa	aaa	caa	aag	aca	agc	aat	ata	gag	act	aat	aat	caa	536
Val	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Ser	Asn	Ile	Glu	Thr	Asn	Asn	Gln	
			150					155					160			
ata	aaa	gta	gaa	caa	gaa	caa	cag	aaa	aca	gaa	caa	gaa	mga	cag	aaa	584
Ile	Lys	Val	Glu	Gln	Glu	Gln	Gln	Lys	Thr	Glu	Gln	Glu	Xaa	Gln	Lys	
		165					170					175				
aca	gaa	caa	gaa	aga	cag	aag	aca	gaa	caa	gaa	aaa	caa	aag	acc	att	632
Thr	Glu	Gln	Glu	Arg	Gln	Lys	Thr	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Ile	
	180					185					190					
aaa	aca	cag	aaa	gat	ttc	att	aaa	tat	gta	gaa	caa	aat	tgc	caa	gaa	680
Lys	Thr	Gln	Lys	Asp	Phe	Ile	Lys	Tyr	Val	Glu	Gln	Asn	Cys	Gln	Glu	
	195				200				205					210		
aat	cat	aat	caa	ttc	ttt	att	gaa	aaa	gga	gga	att	aag	gct	ggt	att	728

Asn	His	Asn	Gln	Phe	Phe	Ile	Glu	Lys	Gly	Gly	Ile	Lys	Ala	Gly	Ile		
				215					220					225			
ggt	ata	gaa	gta	gaa	gct	gaa	tgc	aaa	acc	cct	aaa	cct	gca	aaa	acc	776	
Gly	Ile	Glu	Val	Glu	Ala	Glu	Cys	Lys	Thr	Pro	Lys	Pro	Ala	Lys	Thr		
			230					235					240				
aat	caa	acc	cct	atc	cag	cca	aaa	cac	ctc	cca	aac	tct	aaa	caa	ccc	824	
Asn	Gln	Thr	Pro	Ile	Gln	Pro	Lys	His	Leu	Pro	Asn	Ser	Lys	Gln	Pro		
		245					250				255						
cgc	tct	caa	aga	gga	tca	aaa	gcg	caa	gag	ctt	atc	gct	tat	ttg	caa	872	
Arg	Ser	Gln	Arg	Gly	Ser	Lys	Ala	Gln	Glu	Leu	Ile	Ala	Tyr	Leu	Gln		
	260					265					270						
aaa	gag	cta	gaa	tct	ctg	ccc	tat	tca	caa	aaa	gct	atc	gct	aaa	caa	920	
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gtg	gat	ttt	tat	aga	cca	agt	tct	atc	gct	tat	tta	gaa	cta	gac	cct	968	
Val	Asp	Phe	Tyr	Arg	Pro	Ser	Ser	Ile	Ala	Tyr	Leu	Glu	Leu	Asp	Pro		
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aga	gat	ttt	aat	gtt	aca	gaa	gaa	tgg	caa	aaa	gaa	aat	tta	aaa	ata	1016	
Arg	Asp	Phe	Asn	Val	Thr	Glu	Glu	Trp	Gln	Lys	Glu	Asn	Leu	Lys	Ile		
			310					315					320				
cgc	tct	aaa	gct	caa	gct	aaa	atg	ctt	gaa	atg	agg	agt	tta	aaa	cca	1064	
Arg	Ser	Lys	Ala	Gln	Ala	Lys	Met	Leu	Glu	Met	Arg	Ser	Leu	Lys	Pro		
		325					330					335					
gac	tca	caa	gcc	cac	ctt	tca	acc	tct	caa	agc	ctt	ttg	ttc	gtt	caa	1112	
Asp	Ser	Gln	Ala	His	Leu	Ser	Thr	Ser	Gln	Ser	Leu	Leu	Phe	Val	Gln		
	340					345					350						
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gaa	aag	aaa	gca	gaa	aaa	gcg	ggt	tat	ggt	tat	agt	aaa	agg	atg		1205	
Glu	Lys	Lys	Ala	Glu	Lys	Ala	Gly	Tyr	Gly	Tyr	Ser	Lys	Arg	Met			
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<211> 385

<212> PRT

<213> Helicobacter pylori

<400> 34

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Ser	Thr	Ile	Thr	Asn	Ile	Ile	Arg	Ser	Ile	Arg	Gly	Ile	Phe	Thr	Lys
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Ile	Ala	Lys	Lys	Val	Arg	Gly	Leu	Val	Lys	Lys	His	Pro	Lys	Lys	Ser

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Ser	Ala	Ala	Leu	Val	Val	Leu	Thr	His	Ile	Ala	Cys	Lys	Lys	Ala	Lys
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Glu	Leu	Asp	Asp	Lys	Val	Gln	Asp	Lys	Ser	Lys	Gln	Ala	Glu	Lys	Glu
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Asn	Gln	Ile	Asn	Trp	Trp	Lys	Tyr	Ser	Gly	Leu	Thr	Ile	Ala	Thr	Ser
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Leu	Leu	Leu	Ala	Ala	Cys	Ser	Thr	Gly	Asp	Val	Ser	Glu	Gln	Ile	Glu
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Leu	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Ser	Asn	Ile	Glu	Thr	Asn	Asn	Gln
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Ile	Lys	Val	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Ser	Asn	Ile	Glu	Thr	Asn
145					150					155					160
Asn	Gln	Ile	Lys	Val	Glu	Gln	Glu	Gln	Gln	Lys	Thr	Glu	Gln	Glu	Xaa
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Gln	Lys	Thr	Glu	Gln	Glu	Arg	Gln	Lys	Thr	Glu	Gln	Glu	Lys	Gln	Lys
			180					185					190		
Thr	Ile	Lys	Thr	Gln	Lys	Asp	Phe	Ile	Lys	Tyr	Val	Glu	Gln	Asn	Cys
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Gln	Glu	Asn	His	Asn	Gln	Phe	Phe	Ile	Glu	Lys	Gly	Gly	Ile	Lys	Ala
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Gly	Ile	Gly	Ile	Glu	Val	Glu	Ala	Glu	Cys	Lys	Thr	Pro	Lys	Pro	Ala
225					230					235					240
Lys	Thr	Asn	Gln	Thr	Pro	Ile	Gln	Pro	Lys	His	Leu	Pro	Asn	Ser	Lys
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Gln	Pro	Arg	Ser	Gln	Arg	Gly	Ser	Lys	Ala	Gln	Glu	Leu	Ile	Ala	Tyr
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Leu	Gln	Lys	Glu	Leu	Glu	Ser	Leu	Pro	Tyr	Ser	Gln	Lys	Ala	Ile	Ala
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Lys	Gln	Val	Asp	Phe	Tyr	Arg	Pro	Ser	Ser	Ile	Ala	Tyr	Leu	Glu	Leu
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Asp	Pro	Arg	Asp	Phe	Asn	Val	Thr	Glu	Glu	Trp	Gln	Lys	Glu	Asn	Leu
305				310					315						320
Lys	Ile	Arg	Ser	Lys	Ala	Gln	Ala	Lys	Met	Leu	Glu	Met	Arg	Ser	Leu
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Lys	Pro	Asp	Ser	Gln	Ala	His	Leu	Ser	Thr	Ser	Gln	Ser	Leu	Leu	Phe
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Val	Gln	Lys	Ile	Phe	Ala	Asp	Val	Asn	Lys	Glu	Ile	Lys	Val	Val	Ala
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 <213> Helicobacter pylori

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 Met Lys Lys Gln Ile Leu Thr Gly Val Leu Leu Ser Val Leu Ala Val

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      1           5           10           15
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Ser Ser Ala Tyr Ala His Lys Asp Lys Lys Asp Ala Lys Lys Pro Lys
      20           25           30

ttt agc aca gaa tta gtc gtg gct caa aac gac aaa aaa gac gct aaa 205
Phe Ser Thr Glu Leu Val Val Ala Gln Asn Asp Lys Lys Asp Ala Lys
      35           40           45

aaa cct aaa ttt agc aca gaa tta gtc gtg gct caa aac gac aaa aaa 253
Lys Pro Lys Phe Ser Thr Glu Leu Val Val Ala Gln Asn Asp Lys Lys
      50           55           60

gac gct aaa aaa cct aaa ttt agc aca gaa tta gtc gtg gct caa aac 301
Asp Ala Lys Lys Pro Lys Phe Ser Thr Glu Leu Val Val Ala Gln Asn
      65           70           75           80

gac aaa aaa gac gct aaa aaa cct aaa aac tca gtg gtc taatggcttt 350
Asp Lys Lys Asp Ala Lys Lys Pro Lys Asn Ser Val Val
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<212> PRT
<213> Helicobacter pylori

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      20           25           30
Phe Ser Thr Glu Leu Val Val Ala Gln Asn Asp Lys Lys Asp Ala Lys
      35           40           45
Lys Pro Lys Phe Ser Thr Glu Leu Val Val Ala Gln Asn Asp Lys Lys
      50           55           60
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      65           70           75           80
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      Met Ile Tyr Trp Leu Tyr Leu Ala Val Phe Phe Leu Leu Ser

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Ala Leu Asp Ala	Lys Glu Ile Ala Met	Gln Arg Phe Asp	Lys Gln Asn												
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cat aag att ttt	gaa atc ctt gcg gat	aaa gtg agc gct	aaa gac aat	204											
His Lys Ile Phe	Glu Ile Leu Ala Asp	Lys Val Ser Ala	Lys Asp Asn												
	35	40	45												
gtg ata acc gca	tca ggg aat gcg atc	tta ttg aat tat	gat gtg tat	252											
Val Ile Thr Ala	Ser Gly Asn Ala Ile	Leu Leu Asn Tyr	Asp Val Tyr												
	50	55	60												
att cta gcg gac	aag gtg cgt tat gac	act aaa acc aaa	gaa gcg tta	300											
Ile Leu Ala Asp	Lys Val Arg Tyr Asp	Thr Lys Thr Lys	Glu Ala Leu												
	65	70	75												
tta gag ggg aat	atc aag gtt tat agg	ggc gag ggt ttg	ctc gtt aaa	348											
Leu Glu Gly Asn	Ile Lys Val Tyr Arg	Gly Glu Gly Leu	Leu Val Lys												
	80	85	90												
acc gat tac gtg	aaa ttg agt ttg aat	gaa aaa tat gaa	atc att ttc	396											
Thr Asp Tyr Val	Lys Leu Ser Leu Asn	Glu Lys Tyr Glu	Ile Ile Phe												
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ccc ttt tat gtc	caa gac agc gtg agc	ggg att tgg gtg	agc gcg gat	444											
Pro Phe Tyr Val	Gln Asp Ser Val Ser	Gly Ile Trp Val	Ser Ala Asp												
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Ile Ala Ser Gly	Lys Asp Gln Lys Tyr	Lys Val Lys Asn	Met Ser Thr												
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Ser Gly Cys Ser	Ile Asp Asn Pro Ile	Trp His Val Asn	Ala Thr Ser												
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Gly Ser Phe Asn	Met Gln Lys Ser His	Leu Ser Met Trp	Asn Pro Lys												
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Ile Tyr Val Gly	Asp Ile Pro Val Leu	Tyr Leu Pro Tyr	Ile Phe Met												
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tcc acg agc aat	aaa aga act act ggg	ttt tta tac cct	gag ttt ggc	684											
Ser Thr Ser Asn	Lys Arg Thr Thr Gly	Phe Leu Tyr Pro	Glu Phe Gly												
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act tcc aac tta	gac ggc ttt att tat	ttg caa ccc ttt	tat tta gcc	732											
Thr Ser Asn Leu	Asp Gly Phe Ile Tyr	Leu Gln Pro Phe	Tyr Leu Ala												
	210	215	220												
ccc aaa aac tca	tgg gat atg acc ttt	acc cca caa atc	cgc tat aaa	780											
Pro Lys Asn Ser	Trp Asp Met Thr Phe	Thr Pro Gln Ile	Arg Tyr Lys												
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Arg Gly Phe Gly Leu Asn Phe Glu Ala Arg Tyr Ile Asn Ser Lys Asn	
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Asp Arg Phe Leu Phe Asn Ala Arg Tyr Phe Arg Asn Tyr Thr Gln Tyr	
255 260 265 270	
gtc aaa cgc tac gat ttg agg aat caa aat atc tac ggg ttt gaa ttt	924
Val Lys Arg Tyr Asp Leu Arg Asn Gln Asn Ile Tyr Gly Phe Glu Phe	
275 280 285	
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Leu Ser Ser Ser Arg Asp Thr Leu Gln Lys Tyr Phe His Leu Lys Ser	
290 295 300	
aat att gac aac ggg cat tac att gac ttt tta tac atg aac gat ttg	1020
Asn Ile Asp Asn Gly His Tyr Ile Asp Phe Leu Tyr Met Asn Asp Leu	
305 310 315	
gac tat gtg cgt ttt gaa aag gtt aat aag cgt atc aca gac gcc acg	1068
Asp Tyr Val Arg Phe Glu Lys Val Asn Lys Arg Ile Thr Asp Ala Thr	
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His Met Ser Arg Ala Asn Tyr Tyr Leu Gln Thr Glu Asn Asn Tyr Tyr	
335 340 345 350	
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Gly Leu Asn Ile Lys Tyr Phe Leu Asn Leu Asn Lys Ile Asn Asn Asn	
355 360 365	
cgc act ttc caa tct gtc cct aat ttg caa tac cat aaa tat tta aat	1212
Arg Thr Phe Gln Ser Val Pro Asn Leu Gln Tyr His Lys Tyr Leu Asn	
370 375 380	
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Ser Leu Tyr Phe Arg Asn Leu Leu Tyr Ser Val Asp Tyr Gln Phe Arg	
385 390 395	
aac acc gca aga gag att ggt tat ggc tat gtg caa aac gct ttg aat	1308
Asn Thr Ala Arg Glu Ile Gly Tyr Gly Tyr Val Gln Asn Ala Leu Asn	
400 405 410	
gtg ccg gtg ggc ttg caa ttt tct ttg ttt aaa aag tat ttg tct tta	1356
Val Pro Val Gly Leu Gln Phe Ser Leu Phe Lys Lys Tyr Leu Ser Leu	
415 420 425 430	
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Gly Leu Trp Asn Asp Leu Gln Leu Ser Asn Val Ala Leu Met Gln Ser	
435 440 445	
aaa aat tcc ttc gtg cct acg atc cct aat gaa tca agg gaa ttt ggg	1452
Lys Asn Ser Phe Val Pro Thr Ile Pro Asn Glu Ser Arg Glu Phe Gly	
450 455 460	
aat ttt gtg tct tca aat ttt tcc atg tat gtc aat acg gat ttg gct	1500
Asn Phe Val Ser Ser Asn Phe Ser Met Tyr Val Asn Thr Asp Leu Ala	

465	470	475	
aga gaa tac aac aag ctt ttc cac acg atc caa cta gaa gcg att ttc			1548
Arg Glu Tyr Asn Lys Leu Phe His Thr Ile Gln Leu Glu Ala Ile Phe			
480	485	490	
aac atc cct tat tac acc ttt aaa aac ggc tta ttt tct caa aac atg			1596
Asn Ile Pro Tyr Tyr Thr Phe Lys Asn Gly Leu Phe Ser Gln Asn Met			
495	500	505	510
tat gct tta agc gcg caa gcc tta aac agc tac act tcg cct tta ttg			1644
Tyr Ala Leu Ser Ala Gln Ala Leu Asn Ser Tyr Thr Ser Pro Leu Leu			
	515	520	525
aga gat tat gat tat caa ggg cgt ttg tat gac tcg gtg tgg aat cct			1692
Arg Asp Tyr Asp Tyr Gln Gly Arg Leu Tyr Asp Ser Val Trp Asn Pro			
	530	535	540
agc agt att tta cct agc aat ggc agc aac aag acg gtg gat tta acc			1740
Ser Ser Ile Leu Pro Ser Asn Ala Ser Asn Lys Thr Val Asp Leu Thr			
	545	550	555
cta acg caa tac ctt tat ggc tta ggg ggg caa gag tta ttg tat ttt			1788
Leu Thr Gln Tyr Leu Tyr Gly Leu Gly Gly Gln Glu Leu Leu Tyr Phe			
	560	565	570
aaa ata tcg caa ctc atc aat ctt gac gat aaa gtt tcg ccc ttt aga			1836
Lys Ile Ser Gln Leu Ile Asn Leu Asp Asp Lys Val Ser Pro Phe Arg			
575	580	585	590
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Met Pro Leu Glu Ser Lys Ile Gly Phe Ser Pro Leu Thr Gly Leu Asn			
	595	600	605
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Ile Phe Gly Asn Val Phe Tyr Ser Phe Tyr Gln Asn Arg Leu Glu Glu			
	610	615	620
atc tct gtg aac gcc aat tac caa cgc aag ttt tta agc ttt aac ctc			1980
Ile Ser Val Asn Ala Asn Tyr Gln Arg Lys Phe Leu Ser Phe Asn Leu			
	625	630	635
tct tat ttt tta aaa aac aat ttt agc agt ggg att aat agc att gta			2028
Ser Tyr Phe Leu Lys Asn Asn Phe Ser Ser Gly Ile Asn Ser Ile Val			
	640	645	650
gaa aat ctg cgg att att taaaggcggg ttttagcaac gactttggct			2076
Glu Asn Leu Arg Ile Ile			
655	660		
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Tyr	Val	Lys	Leu	Ser	Leu	Asn	Glu	Lys	Tyr	Glu	Ile	Ile	Phe	Pro	Phe
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Tyr	Val	Gln	Asp	Ser	Val	Ser	Gly	Ile	Trp	Val	Ser	Ala	Asp	Ile	Ala
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Cys	Ser	Ile	Asp	Asn	Pro	Ile	Trp	His	Val	Asn	Ala	Thr	Ser	Gly	Ser
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Phe	Asn	Met	Gln	Lys	Ser	His	Leu	Ser	Met	Trp	Asn	Pro	Lys	Ile	Tyr
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Ser	Arg	Ala	Asn	Tyr	Tyr	Leu	Gln	Thr	Glu	Asn	Asn	Tyr	Tyr	Gly	Leu
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Ala	Arg	Glu	Ile	Gly	Tyr	Gly	Tyr	Val	Gln	Asn	Ala	Leu	Asn	Val	Pro
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Val	Gly	Leu	Gln	Phe	Ser	Leu	Phe	Lys	Lys	Tyr	Leu	Ser	Leu	Gly	Leu
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Val	Ser	Ser	Asn	Phe	Ser	Met	Tyr	Val	Asn	Thr	Asp	Leu	Ala	Arg	Glu	
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Pro	Tyr	Tyr	Thr	Phe	Lys	Asn	Gly	Leu	Phe	Ser	Gln	Asn	Met	Tyr	Ala	
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Gly	Asn	Val	Phe	Tyr	Ser	Phe	Tyr	Gln	Asn	Arg	Leu	Glu	Glu	Ile	Ser	
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Val	Asn	Ala	Asn	Tyr	Gln	Arg	Lys	Phe	Leu	Ser	Phe	Asn	Leu	Ser	Tyr	
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Phe	Leu	Lys	Asn	Asn	Phe	Ser	Ser	Gly	Ile	Asn	Ser	Ile	Val	Glu	Asn	
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Leu	Arg	Ile	Ile													
			660													

<210> 39
 <211> 961
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (168)...(764)

<400> 39
 atgccgatta aatgcatgct gattaaatga atgaaaagag tccaaaccac cgcctttaac 60
 gcaccacgct tgaaattaaa actaaatttt agtgatttct tagcaaattt tagataagat 120
 caagcgtgat tttttctaaa ttttaggcatt ttaaggaatc agtgttt atg aca agc 176
 Met Thr Ser
 1

gct	ctg	tta	ggc	tta	caa	att	gtt	tta	gcg	gta	ttg	att	gtg	gtg	gtg	224
Ala	Leu	Leu	Gly	Leu	Gln	Ile	Val	Leu	Ala	Val	Leu	Ile	Val	Val	Val	
5						10					15					

gtt	ttg	ttg	caa	aaa	agt	tct	agc	atc	ggc	tta	ggg	gct	tat	agc	ggg	272
Val	Leu	Leu	Gln	Lys	Ser	Ser	Ser	Ile	Gly	Leu	Gly	Ala	Tyr	Ser	Gly	
20					25				30						35	

agt	aat	gag	tct	tta	ttt	ggc	gct	aaa	ggg	cct	gca	agc	ttt	atg	gcg	320
Ser	Asn	Glu	Ser	Leu	Phe	Gly	Ala	Lys	Gly	Pro	Ala	Ser	Phe	Met	Ala	
				40					45					50		

aaa	tta	acc	atg	ttt	tta	ggg	ctg	tta	ttt	gtc	atc	aac	acc	atc	gct	368
Lys	Leu	Thr	Met	Phe	Leu	Gly	Leu	Leu	Phe	Val	Ile	Asn	Thr	Ile	Ala	

55										60					65					
ttg ggc tat ttt tac aac aaa gaa tac ggc aag agc gtt tta gat gag	416																			
Leu Gly Tyr Phe Tyr Asn Lys Glu Tyr Gly Lys Ser Val Leu Asp Glu																				
70 75 80																				
act aaa acc aac aaa gaa ctt tcg ccc cta gtc cct gcc acc ggc acg	464																			
Thr Lys Thr Asn Lys Glu Leu Ser Pro Leu Val Pro Ala Thr Gly Thr																				
85 90 95																				
ctt aac cct gca ctt aat ccc aca tta aac cca acg ctc aac cct tta	512																			
Leu Asn Pro Ala Leu Asn Pro Thr Leu Asn Pro Thr Leu Asn Pro Leu																				
100 105 110 115																				
gag caa gcc cca act aat cct tta atg cca caa caa acg cct aac gaa	560																			
Glu Gln Ala Pro Thr Asn Pro Leu Met Pro Gln Gln Thr Pro Asn Glu																				
120 125 130																				
ctc cct aaa gag cca gcc aaa acg cct tct gtt gaa agc ccc aaa cag	608																			
Leu Pro Lys Glu Pro Ala Lys Thr Pro Ser Val Glu Ser Pro Lys Gln																				
135 140 145																				
aat gaa aag aat gaa aag aat gac gcc aaa gag aat ggt ata aag ggt	656																			
Asn Glu Lys Asn Glu Lys Asn Asp Ala Lys Glu Asn Gly Ile Lys Gly																				
150 155 160																				
gtt gaa aaa acc aaa gag aac gcc aaa acg ccc cca acc acc cac caa	704																			
Val Glu Lys Thr Lys Glu Asn Ala Lys Thr Pro Pro Thr Thr His Gln																				
165 170 175																				
aag cct aaa acg cat gca acg caa acc aac gcc cat acc aac caa aaa	752																			
Lys Pro Lys Thr His Ala Thr Gln Thr Asn Ala His Thr Asn Gln Lys																				
180 185 190 195																				
aag gat gaa aaa taatgttaca ggccatttat aacgaaacca aagatctgat	804																			
Lys Asp Glu Lys																				
gcaaaaaagc attcaagctt taaacagggg tttttccact ctaaggagcg cgaaagtttc 864																				
agtcaatatt ttagatcaca tcaaagtggg ttattacggc acgcccacgg cattaaatca 924																				
agtcggatcc gtgatgagct tggatgcgac caccctt 961																				

<210> 40

<211> 199

<212> PRT

<213> Helicobacter pylori

<400> 40

Met Thr Ser Ala Leu Leu Gly Leu Gln Ile Val Leu Ala Val Leu Ile	
1 5 10 15	
Val Val Val Val Leu Leu Gln Lys Ser Ser Ser Ile Gly Leu Gly Ala	
20 25 30	
Tyr Ser Gly Ser Asn Glu Ser Leu Phe Gly Ala Lys Gly Pro Ala Ser	
35 40 45	
Phe Met Ala Lys Leu Thr Met Phe Leu Gly Leu Leu Phe Val Ile Asn	
50 55 60	
Thr Ile Ala Leu Gly Tyr Phe Tyr Asn Lys Glu Tyr Gly Lys Ser Val	
65 70 75 80	

Leu Asp Glu Thr Lys Thr Asn Lys Glu Leu Ser Pro Leu Val Pro Ala
 85 90 95
 Thr Gly Thr Leu Asn Pro Ala Leu Asn Pro Thr Leu Asn Pro Thr Leu
 100 105 110
 Asn Pro Leu Glu Gln Ala Pro Thr Asn Pro Leu Met Pro Gln Gln Thr
 115 120 125
 Pro Asn Glu Leu Pro Lys Glu Pro Ala Lys Thr Pro Ser Val Glu Ser
 130 135 140
 Pro Lys Gln Asn Glu Lys Asn Glu Lys Asn Asp Ala Lys Glu Asn Gly
 145 150 155 160
 Ile Lys Gly Val Glu Lys Thr Lys Glu Asn Ala Lys Thr Pro Pro Thr
 165 170 175
 Thr His Gln Lys Pro Lys Thr His Ala Thr Gln Thr Asn Ala His Thr
 180 185 190
 Asn Gln Lys Lys Asp Glu Lys
 195

<210> 41
 <211> 1058
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (325)...(879)

<400> 41
 cctagtcctt gccaccggca cgcttaaccc tgcacttaat cccacattaa acccaacgct 60
 caacccttta gagcaagccc caactaatcc tttaatgcc caacaaacgc ctaacgaact 120
 ccctaaagag ccagccaaaa cgccttctgt tgaaagcccc aaacagaatg aaaagaatga 180
 aaagaatgac gccaaagaga atggtataaa ggggtgttgaa aaaaccaaag agaacgcca 240
 aacgccccca accaccacc aaaagcctaa aacgcattgca acgcaaacca acgcccatac 300
 caaccaaaaa aaggatgaaa aata atg tta cag gcc att tat aac gaa acc 351
 Met Leu Gln Ala Ile Tyr Asn Glu Thr
 1 5
 aaa gat ctg atg caa aaa agc att caa gct tta aac agg gat ttt tcc 399
 Lys Asp Leu Met Gln Lys Ser Ile Gln Ala Leu Asn Arg Asp Phe Ser
 10 15 20 25
 act cta agg agc gcg aaa gtt tca gtc aat att tta gat cac atc aaa 447
 Thr Leu Arg Ser Ala Lys Val Ser Val Asn Ile Leu Asp His Ile Lys
 30 35 40
 gtg gat tat tac ggc acg ccc acg gca tta aat caa gtc gga tcc gtg 495
 Val Asp Tyr Tyr Gly Thr Pro Thr Ala Leu Asn Gln Val Gly Ser Val
 45 50 55
 atg agc ttg gat gcg acc acc ctt caa atc agc cca tgg gaa aaa aac 543
 Met Ser Leu Asp Ala Thr Thr Leu Gln Ile Ser Pro Trp Glu Lys Asn
 60 65 70
 ctg ctc aaa gaa att gaa aga tcc att caa gaa gcc aat att ggt gtc 591
 Leu Leu Lys Glu Ile Glu Arg Ser Ile Gln Glu Ala Asn Ile Gly Val
 75 80 85
 aat cct aat aac gac ggc gaa acg atc aag ctt ttt ttc ccg ccc atg 639

Asn	Pro	Asn	Asn	Asp	Gly	Glu	Thr	Ile	Lys	Leu	Phe	Phe	Pro	Pro	Met	
90					95					100					105	
aca	agt	gag	caa	aga	aaa	ctc	atc	gca	aaa	gac	gcc	aaa	gcg	atg	ggc	687
Thr	Ser	Glu	Gln	Arg	Lys	Leu	Ile	Ala	Lys	Asp	Ala	Lys	Ala	Met	Gly	
				110					115					120		
gaa	aag	gct	aaa	gtg	gct	gtg	agg	aat	atc	cgc	caa	gat	gct	aac	aac	735
Glu	Lys	Ala	Lys	Val	Ala	Val	Arg	Asn	Ile	Arg	Gln	Asp	Ala	Asn	Asn	
			125					130					135			
cag	gtg	aaa	aaa	tta	gaa	aaa	gac	aaa	gaa	atc	agc	gaa	gat	gaa	agc	783
Gln	Val	Lys	Lys	Leu	Glu	Lys	Asp	Lys	Glu	Ile	Ser	Glu	Asp	Glu	Ser	
		140					145					150				
aaa	aaa	gcc	caa	gag	cag	atc	caa	aaa	atc	acc	gat	gaa	gcc	att	aaa	831
Lys	Lys	Ala	Gln	Glu	Gln	Ile	Gln	Lys	Ile	Thr	Asp	Glu	Ala	Ile	Lys	
		155				160					165					
aaa	att	gat	gaa	agc	gtg	aaa	aac	aaa	gaa	gac	gcg	atc	tta	aag	gtc	879
Lys	Ile	Asp	Glu	Ser	Val	Lys	Asn	Lys	Glu	Asp	Ala	Ile	Leu	Lys	Val	
170					175					180					185	
taaaccatgg atattaaggc atgttatcaa aacgctaaag cggtattaga ggggcatttc 939																
ttgctcagca gtgggtttca ttccaattat tatttgcaat ccgctaaagt tttagaagat 999																
cccaaactag ccgaacaatt agcgctagaa ttagccaaac aaatccaaga agctcattt 1058																

<210> 42
 <211> 185
 <212> PRT
 <213> Helicobacter pylori

<400> 42															
Met	Leu	Gln	Ala	Ile	Tyr	Asn	Glu	Thr	Lys	Asp	Leu	Met	Gln	Lys	Ser
1				5					10					15	
Ile	Gln	Ala	Leu	Asn	Arg	Asp	Phe	Ser	Thr	Leu	Arg	Ser	Ala	Lys	Val
			20					25					30		
Ser	Val	Asn	Ile	Leu	Asp	His	Ile	Lys	Val	Asp	Tyr	Tyr	Gly	Thr	Pro
		35				40					45				
Thr	Ala	Leu	Asn	Gln	Val	Gly	Ser	Val	Met	Ser	Leu	Asp	Ala	Thr	Thr
	50					55					60				
Leu	Gln	Ile	Ser	Pro	Trp	Glu	Lys	Asn	Leu	Leu	Lys	Glu	Ile	Glu	Arg
65					70				75						80
Ser	Ile	Gln	Glu	Ala	Asn	Ile	Gly	Val	Asn	Pro	Asn	Asn	Asp	Gly	Glu
				85					90					95	
Thr	Ile	Lys	Leu	Phe	Phe	Pro	Pro	Met	Thr	Ser	Glu	Gln	Arg	Lys	Leu
			100					105					110		
Ile	Ala	Lys	Asp	Ala	Lys	Ala	Met	Gly	Glu	Lys	Ala	Lys	Val	Ala	Val
		115					120					125			
Arg	Asn	Ile	Arg	Gln	Asp	Ala	Asn	Asn	Gln	Val	Lys	Lys	Leu	Glu	Lys
		130				135					140				
Asp	Lys	Glu	Ile	Ser	Glu	Asp	Glu	Ser	Lys	Lys	Ala	Gln	Glu	Gln	Ile
145					150					155					160
Gln	Lys	Ile	Thr	Asp	Glu	Ala	Ile	Lys	Lys	Ile	Asp	Glu	Ser	Val	Lys
			165					170						175	
Asn	Lys	Glu	Asp	Ala	Ile	Leu	Lys	Val							
			180					185							

<210> 43
 <211> 1669
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (163)...(1389)

<400> 43
 gagtggatga aaaagacact ttcaattttg caaaaattgg ctatgaacag ggcaagggcg 60
 aagaattaaa agaagtagaa gaaaagcatg cgtttaagaa aatccctttt gtcaaagatt 120
 tgcacaaaat cgccccact atcttaaaaa agaggctata aa atg gct caa aat 174
 Met Ala Gln Asn
 1

ttc acg aaa ctc aac ccc cag ttt gaa aac atc att ttt gaa cat gac 222
 Phe Thr Lys Leu Asn Pro Gln Phe Glu Asn Ile Ile Phe Glu His Asp
 5 10 15 20

gac aac caa atg att tta aac ttt ggc ccc caa cac ccc agt agt cat 270
 Asp Asn Gln Met Ile Leu Asn Phe Gly Pro Gln His Pro Ser Ser His
 25 30 35

ggg caa ttg cgc ttg att ttg gaa tta gag ggc gaa aaa atc att aag 318
 Gly Gln Leu Arg Leu Ile Leu Glu Leu Glu Gly Glu Lys Ile Ile Lys
 40 45 50

gct acc cct gaa att ggc tac ttg cat aga ggc tgt gaa aag tta ggc 366
 Ala Thr Pro Glu Ile Gly Tyr Leu His Arg Gly Cys Glu Lys Leu Gly
 55 60 65

gaa aac atg acc tat aac gaa tac atg ccc act act gat aga ttg gat 414
 Glu Asn Met Thr Tyr Asn Glu Tyr Met Pro Thr Thr Asp Arg Leu Asp
 70 75 80

tac act tct tct acc agc aat aat tac gct tac gct tat gcg gta gag 462
 Tyr Thr Ser Ser Thr Ser Asn Asn Tyr Ala Tyr Ala Tyr Ala Val Glu
 85 90 95 100

acc tta ctc aat tta gaa atc cca cgc cga gcg cag gtg atc cgc acg 510
 Thr Leu Leu Asn Leu Glu Ile Pro Arg Arg Ala Gln Val Ile Arg Thr
 105 110 115

att tta cta gag ctt aac cgc atg atc tca cac atc ttt ttt atc agc 558
 Ile Leu Leu Glu Leu Asn Arg Met Ile Ser His Ile Phe Phe Ile Ser
 120 125 130

gtg cat gct tta gat gtg ggg gcg atg agc gtg ttt ttg tat gcg ttt 606
 Val His Ala Leu Asp Val Gly Ala Met Ser Val Phe Leu Tyr Ala Phe
 135 140 145

aaa acg agg gaa tac ggc ttg gat ttg atg gag gat tat tgc ggg gct 654
 Lys Thr Arg Glu Tyr Gly Leu Asp Leu Met Glu Asp Tyr Cys Gly Ala
 150 155 160

agg ctc acg cat aac gct ata agg att ggg ggc gtg cct tta gat tta 702
 Arg Leu Thr His Asn Ala Ile Arg Ile Gly Gly Val Pro Leu Asp Leu

165	170	175	180	
ccc cct aat tgg tta gaa ggc tta aaa aag ttt tta ggc gaa atg agg				750
Pro Pro Asn Trp Leu Glu Gly Leu Lys Lys Phe Leu Gly Glu Met Arg	185	190	195	
gaa tgc aaa aaa ctc att caa ggc tta ttg gat aag aat cgc att tgg				798
Glu Cys Lys Lys Leu Ile Gln Gly Leu Leu Asp Lys Asn Arg Ile Trp	200	205	210	
cgg atg cgc ttg gaa aat gtg ggc gtt gta acg caa aaa atg gcg caa				846
Arg Met Arg Leu Glu Asn Val Gly Val Val Thr Gln Lys Met Ala Gln	215	220	225	
agc tgg ggc atg agc ggt atc atg tta aga ggg act ggg atc gct tat				894
Ser Trp Gly Met Ser Gly Ile Met Leu Arg Gly Thr Gly Ile Ala Tyr	230	235	240	
gac atc aga aaa gaa gag cct tat gag ctt tat aaa gag ctt gat ttt				942
Asp Ile Arg Lys Glu Glu Pro Tyr Glu Leu Tyr Lys Glu Leu Asp Phe	245	250	255	260
gat gtg ccg gtg ggc aat tat ggc gat agt tat gat agg tat tgt ttg				990
Asp Val Pro Val Gly Asn Tyr Gly Asp Ser Tyr Asp Arg Tyr Cys Leu	265	270	275	
tat atg tta gaa att gat gaa agc gtt cgc atc att gaa cag ctc att				1038
Tyr Met Leu Glu Ile Asp Glu Ser Val Arg Ile Ile Glu Gln Leu Ile	280	285	290	
cct atg tat gct aaa acc gat acg cct atc atg gct caa aac ccg cat				1086
Pro Met Tyr Ala Lys Thr Asp Thr Pro Ile Met Ala Gln Asn Pro His	295	300	305	
tat att tcc gcc cct aaa gaa gat ata atg acg caa aac tac gcc ttg				1134
Tyr Ile Ser Ala Pro Lys Glu Asp Ile Met Thr Gln Asn Tyr Ala Leu	310	315	320	
atg cag cat ttt gtt tta gtg gct cag ggc atg cgt ccg ccc gtt ggg				1182
Met Gln His Phe Val Leu Val Ala Gln Gly Met Arg Pro Pro Val Gly	325	330	335	340
gaa gtg tat gcc ccc aca gaa agc cct aaa ggg gaa tta ggg ttt ttt				1230
Glu Val Tyr Ala Pro Thr Glu Ser Pro Lys Gly Glu Leu Gly Phe Phe	345	350	355	
atc cat tca gag ggc gag cct tac cct cac agg cta aaa atc aga gcc				1278
Ile His Ser Glu Gly Glu Pro Tyr Pro His Arg Leu Lys Ile Arg Ala	360	365	370	
cct agc ttt tat cac att ggg gct ttg agc gac att tta gtg ggg caa				1326
Pro Ser Phe Tyr His Ile Gly Ala Leu Ser Asp Ile Leu Val Gly Gln	375	380	385	
tat tta gcg gat gca gta acc gtg att ggc tca acc aat gcg gtg ttt				1374
Tyr Leu Ala Asp Ala Val Thr Val Ile Gly Ser Thr Asn Ala Val Phe	390	395	400	

ggc gag gtg gat aga tgaaacgctt tgatttacgc cccttaaaag cgggtatttt 1429
 Gly Glu Val Asp Arg
 405

tgaacgctta gaagaattga ttgaaaaaga aatgcaacct aatgaagtcg ctattttcat 1489
 gtttgaagtg ggggattttt ctaatatccc taagagcgct gaatttatcc aatctaaagg 1549
 gcatgagctc ctcaattctt tgcgtttcaa tcaagcggat tggacgattg tcgtgagaaa 1609
 aaaggcttga ttttgagcgg ctttaacccc ttaaattctc ccttagtcgc aagctcttct 1669

<210> 44
 <211> 409
 <212> PRT
 <213> Helicobacter pylori

<400> 44
 Met Ala Gln Asn Phe Thr Lys Leu Asn Pro Gln Phe Glu Asn Ile Ile
 1 5 10 15
 Phe Glu His Asp Asp Asn Gln Met Ile Leu Asn Phe Gly Pro Gln His
 20 25 30
 Pro Ser Ser His Gly Gln Leu Arg Leu Ile Leu Glu Leu Glu Gly Glu
 35 40 45
 Lys Ile Ile Lys Ala Thr Pro Glu Ile Gly Tyr Leu His Arg Gly Cys
 50 55 60
 Glu Lys Leu Gly Glu Asn Met Thr Tyr Asn Glu Tyr Met Pro Thr Thr
 65 70 75 80
 Asp Arg Leu Asp Tyr Thr Ser Ser Thr Ser Asn Asn Tyr Ala Tyr Ala
 85 90 95
 Tyr Ala Val Glu Thr Leu Leu Asn Leu Glu Ile Pro Arg Arg Ala Gln
 100 105 110
 Val Ile Arg Thr Ile Leu Leu Glu Leu Asn Arg Met Ile Ser His Ile
 115 120 125
 Phe Phe Ile Ser Val His Ala Leu Asp Val Gly Ala Met Ser Val Phe
 130 135 140
 Leu Tyr Ala Phe Lys Thr Arg Glu Tyr Gly Leu Asp Leu Met Glu Asp
 145 150 155 160
 Tyr Cys Gly Ala Arg Leu Thr His Asn Ala Ile Arg Ile Gly Gly Val
 165 170 175
 Pro Leu Asp Leu Pro Pro Asn Trp Leu Glu Gly Leu Lys Lys Phe Leu
 180 185 190
 Gly Glu Met Arg Glu Cys Lys Lys Leu Ile Gln Gly Leu Leu Asp Lys
 195 200 205
 Asn Arg Ile Trp Arg Met Arg Leu Glu Asn Val Gly Val Val Thr Gln
 210 215 220
 Lys Met Ala Gln Ser Trp Gly Met Ser Gly Ile Met Leu Arg Gly Thr
 225 230 235 240
 Gly Ile Ala Tyr Asp Ile Arg Lys Glu Glu Pro Tyr Glu Leu Tyr Lys
 245 250 255
 Glu Leu Asp Phe Asp Val Pro Val Gly Asn Tyr Gly Asp Ser Tyr Asp
 260 265 270
 Arg Tyr Cys Leu Tyr Met Leu Glu Ile Asp Glu Ser Val Arg Ile Ile
 275 280 285
 Glu Gln Leu Ile Pro Met Tyr Ala Lys Thr Asp Thr Pro Ile Met Ala
 290 295 300
 Gln Asn Pro His Tyr Ile Ser Ala Pro Lys Glu Asp Ile Met Thr Gln
 305 310 315 320
 Asn Tyr Ala Leu Met Gln His Phe Val Leu Val Ala Gln Gly Met Arg
 325 330 335

Pro Pro Val Gly Glu Val Tyr Ala Pro Thr Glu Ser Pro Lys Gly Glu
 340 345 350
 Leu Gly Phe Phe Ile His Ser Glu Gly Glu Pro Tyr Pro His Arg Leu
 355 360 365
 Lys Ile Arg Ala Pro Ser Phe Tyr His Ile Gly Ala Leu Ser Asp Ile
 370 375 380
 Leu Val Gly Gln Tyr Leu Ala Asp Ala Val Thr Val Ile Gly Ser Thr
 385 390 395 400
 Asn Ala Val Phe Gly Glu Val Asp Arg
 405

<210> 45
 <211> 869
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (358)...(732)

<400> 45
 taacttgtgg ttaactaccg ccagactcct tttgagtttg gcaaacgcg caatgagttc 60
 tttaggcatt ttttcagtgc cgatcttaaa gttttcaaga ctgcgttgcg tttgagcccc 120
 ccaatattgg ctatcattta ctttgatttc gcccatcggt tcatgttcaa ttctaaattg 180
 catgctaata ctttgaaatt tgatttttaa accttaaaaa aatagcataa actcttatac 240
 cttctactta aaaaccctaa ttttttaaac accattttcca caatttttac acaaaagagg 300
 gttattatcc gttcgcaaca agaattttct tgttatctta atgtaaaggt' caaaacg atg 360
 Met
 1

aaa aag tta gcc gct tta ttt tta gta agc gtg ttg ggg gtt atg ggt 408
 Lys Lys Leu Ala Ala Leu Phe Leu Val Ser Val Leu Gly Val Met Gly
 5 10 15

tta aac gca tgg gag caa acc cta aaa gct aat gac ttg gaa gtg aaa 456
 Leu Asn Ala Trp Glu Gln Thr Leu Lys Ala Asn Asp Leu Glu Val Lys
 20 25 30

atc aaa tcc gtg ggt aac ccc att aaa ggc gat aac act ttc att ctc 504
 Ile Lys Ser Val Gly Asn Pro Ile Lys Gly Asp Asn Thr Phe Ile Leu
 35 40 45

agc ccc act tta aaa ggt aag gct tta gaa aaa gct atc gtt agg gtg 552
 Ser Pro Thr Leu Lys Gly Lys Ala Leu Glu Lys Ala Ile Val Arg Val
 50 55 60 65

cag ttt atg atg cct gaa atg ccc ggc atg cca gcg atg aaa gaa atg 600
 Gln Phe Met Met Pro Glu Met Pro Gly Met Pro Ala Met Lys Glu Met
 70 75 80

gcg caa gtg agt gaa aaa aac ggc ctt tat gaa gct aaa acc aat ctt 648
 Ala Gln Val Ser Glu Lys Asn Gly Leu Tyr Glu Ala Lys Thr Asn Leu
 85 90 95

tct atg aac ggg aca tgg cag gtt agg gtg gat att aaa tct aaa gag 696
 Ser Met Asn Gly Thr Trp Gln Val Arg Val Asp Ile Lys Ser Lys Glu
 100 105 110

ggt cag gtt tat cgc gct aaa aca agc ctg gat tta taagagcatg 742
 Gly Gln Val Tyr Arg Ala Lys Thr Ser Leu Asp Leu
 115 120 125

ctatcttttta taagcgcggtt tgataaaagg ggcgtttcaa tacgcctttt aacagccttg 802
 ttactgctttt ttagtttggg tttggctaaa gatttagaga tccaatcttt tgtggctaaa 862
 taccttt 869

<210> 46
 <211> 125
 <212> PRT
 <213> Helicobacter pylori

<400> 46
 Met Lys Lys Leu Ala Ala Leu Phe Leu Val Ser Val Leu Gly Val Met
 1 5 10 15
 Gly Leu Asn Ala Trp Glu Gln Thr Leu Lys Ala Asn Asp Leu Glu Val
 20 25 30
 Lys Ile Lys Ser Val Gly Asn Pro Ile Lys Gly Asp Asn Thr Phe Ile
 35 40 45
 Leu Ser Pro Thr Leu Lys Gly Lys Ala Leu Glu Lys Ala Ile Val Arg
 50 55 60
 Val Gln Phe Met Met Pro Glu Met Pro Gly Met Pro Ala Met Lys Glu
 65 70 75 80
 Met Ala Gln Val Ser Glu Lys Asn Gly Leu Tyr Glu Ala Lys Thr Asn
 85 90 95
 Leu Ser Met Asn Gly Thr Trp Gln Val Arg Val Asp Ile Lys Ser Lys
 100 105 110
 Glu Gly Gln Val Tyr Arg Ala Lys Thr Ser Leu Asp Leu
 115 120 125

<210> 47
 <211> 1217
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (73)...(1152)

<400> 47
 tccatgcggtt ttgatgcgat tttaaaaaat ctttgggtat tttagcatgc caatgggttaa 60
 aaaaagggtgg tt atg aat ggt ttt tgc gct aga cta cga gcc ata act cat 111
 Met Asn Gly Phe Cys Ala Arg Leu Arg Ala Ile Thr His
 1 5 10

aat gaa aga tta aaa atg aaa ata gcg gta tta ctc agt ggg ggg gtg 159
 Asn Glu Arg Leu Lys Met Lys Ile Ala Val Leu Leu Ser Gly Gly Val
 15 20 25

gat agc tct tat agc gct tat agc tta aaa gag caa ggg cat gaa tta 207
 Asp Ser Ser Tyr Ser Ala Tyr Ser Leu Lys Glu Gln Gly His Glu Leu
 30 35 40 45

gtg ggg att tat tta aaa ctc cat gcg agt gaa aaa aag cat gat tta 255
 Val Gly Ile Tyr Leu Lys Leu His Ala Ser Glu Lys Lys His Asp Leu

50										55					60					
tac	atc	aaa	aac	gct	caa	aaa	gca	tgc	gag	ttt	tta	ggc	att	cct	tta	303				
Tyr	Ile	Lys	Asn	Ala	Gln	Lys	Ala	Cys	Glu	Phe	Leu	Gly	Ile	Pro	Leu					
			65					70					75							
gag	gtg	ttg	gat	ttt	caa	aag	gat	ttt	aaa	agc	gcg	gtt	tat	gat	gaa	351				
Glu	Val	Leu	Asp	Phe	Gln	Lys	Asp	Phe	Lys	Ser	Ala	Val	Tyr	Asp	Glu					
		80					85					90								
ttt	atc	aac	gcc	tat	gaa	gaa	ggg	caa	acc	cca	aac	cct	tgt	gcg	ttg	399				
Phe	Ile	Asn	Ala	Tyr	Glu	Glu	Gly	Gln	Thr	Pro	Asn	Pro	Cys	Ala	Leu					
	95					100					105									
tgc	aac	cct	tta	atg	aag	ttt	ggg	cta	gct	ttg	gat	cac	gct	tta	aaa	447				
Cys	Asn	Pro	Leu	Met	Lys	Phe	Gly	Leu	Ala	Leu	Asp	His	Ala	Leu	Lys					
110					115				120					125						
tta	ggg	tgt	gaa	aag	atc	gct	acc	ggg	cat	tat	gcg	aga	gtc	aaa	gaa	495				
Leu	Gly	Cys	Glu	Lys	Ile	Ala	Thr	Gly	His	Tyr	Ala	Arg	Val	Lys	Glu					
				130				135					140							
att	gac	aaa	ata	agt	tat	att	caa	gag	gct	ttg	gat	aaa	act	aaa	gat	543				
Ile	Asp	Lys	Ile	Ser	Tyr	Ile	Gln	Glu	Ala	Leu	Asp	Lys	Thr	Lys	Asp					
			145					150					155							
cag	agc	tat	ttt	tta	tac	gct	tta	gag	cat	gaa	gtg	atc	gct	aaa	ttg	591				
Gln	Ser	Tyr	Phe	Leu	Tyr	Ala	Leu	Glu	His	Glu	Val	Ile	Ala	Lys	Leu					
		160				165					170									
gtg	ttc	cct	tta	ggg	gat	ttg	cta	aaa	aag	gat	att	aag	cct	tta	gcc	639				
Val	Phe	Pro	Leu	Gly	Asp	Leu	Leu	Lys	Lys	Asp	Ile	Lys	Pro	Leu	Ala					
	175					180					185									
ttg	aat	gcg	atg	cct	ttt	tta	ggc	act	tta	gag	act	tat	aag	gaa	tct	687				
Leu	Asn	Ala	Met	Pro	Phe	Leu	Gly	Thr	Leu	Glu	Thr	Tyr	Lys	Glu	Ser					
190					195					200				205						
caa	gaa	atc	tgc	ttt	gtg	gaa	aaa	agc	tac	att	gac	act	tta	aaa	aag	735				
Gln	Glu	Ile	Cys	Phe	Val	Glu	Lys	Ser	Tyr	Ile	Asp	Thr	Leu	Lys	Lys					
				210					215					220						
cat	gtt	gaa	gtg	gaa	aaa	gag	ggc	gtg	gtg	aaa	aac	cta	caa	ggc	gaa	783				
His	Val	Glu	Val	Glu	Lys	Glu	Gly	Val	Val	Lys	Asn	Leu	Gln	Gly	Glu					
			225				230						235							
gtc	att	ggc	acg	cat	aaa	ggc	tat	atg	caa	tac	acg	att	ggc	aaa	cgc	831				
Val	Ile	Gly	Thr	His	Lys	Gly	Tyr	Met	Gln	Tyr	Thr	Ile	Gly	Lys	Arg					
		240				245						250								
aaa	ggc	ttt	agt	att	aaa	ggc	gcg	tta	gag	ccg	cat	ttt	gtg	gtg	ggg	879				
Lys	Gly	Phe	Ser	Ile	Lys	Gly	Ala	Leu	Glu	Pro	His	Phe	Val	Val	Gly					
	255					260					265									
att	gac	gct	aaa	aag	aac	gag	cta	gtc	gtg	ggc	aaa	aaa	gaa	gat	ctc	927				
Ile	Asp	Ala	Lys	Lys	Asn	Glu	Leu	Val	Val	Gly	Lys	Lys	Glu	Asp	Leu					
270					275					280					285					

gcc acg cat tcg ctt aag gct aaa aac aaa tct tta atg aaa gat ttt 975
 Ala Thr His Ser Leu Lys Ala Lys Asn Lys Ser Leu Met Lys Asp Phe
 290 295 300

aaa gat ggc gaa tat ttt atc aag gct cgt tac agg agc gtg cct gct 1023
 Lys Asp Gly Glu Tyr Phe Ile Lys Ala Arg Tyr Arg Ser Val Pro Ala
 305 310 315

aaa gcg cat gtg agt ttg aaa gat gag gtg att gaa gtg ggg ttt aaa 1071
 Lys Ala His Val Ser Leu Lys Asp Glu Val Ile Glu Val Gly Phe Lys
 320 325 330

gag cct ttt tat ggc gtg gct aaa ggg caa gct ttg gtc gtt tat aaa 1119
 Glu Pro Phe Tyr Gly Val Ala Lys Gly Gln Ala Leu Val Val Tyr Lys
 335 340 345

gat gac atc ttg ctt ggt ggg ggc gtg att gtt taaaaactaa agaactaaga 1172
 Asp Asp Ile Leu Leu Gly Gly Gly Val Ile Val
 350 355 360

gatacgccctt ttggcagtcct cttaatgttt tattgaatag gcggtt 1217

<210> 48
 <211> 360
 <212> PRT
 <213> Helicobacter pylori

<400> 48
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 Leu Lys Met Lys Ile Ala Val Leu Leu Ser Gly Gly Val Asp Ser Ser
 20 25 30
 Tyr Ser Ala Tyr Ser Leu Lys Glu Gln Gly His Glu Leu Val Gly Ile
 35 40 45
 Tyr Leu Lys Leu His Ala Ser Glu Lys Lys His Asp Leu Tyr Ile Lys
 50 55 60
 Asn Ala Gln Lys Ala Cys Glu Phe Leu Gly Ile Pro Leu Glu Val Leu
 65 70 75 80
 Asp Phe Gln Lys Asp Phe Lys Ser Ala Val Tyr Asp Glu Phe Ile Asn
 85 90 95
 Ala Tyr Glu Glu Gly Gln Thr Pro Asn Pro Cys Ala Leu Cys Asn Pro
 100 105 110
 Leu Met Lys Phe Gly Leu Ala Leu Asp His Ala Leu Lys Leu Gly Cys
 115 120 125
 Glu Lys Ile Ala Thr Gly His Tyr Ala Arg Val Lys Glu Ile Asp Lys
 130 135 140
 Ile Ser Tyr Ile Gln Glu Ala Leu Asp Lys Thr Lys Asp Gln Ser Tyr
 145 150 155 160
 Phe Leu Tyr Ala Leu Glu His Glu Val Ile Ala Lys Leu Val Phe Pro
 165 170 175
 Leu Gly Asp Leu Leu Lys Lys Asp Ile Lys Pro Leu Ala Leu Asn Ala
 180 185 190
 Met Pro Phe Leu Gly Thr Leu Glu Thr Tyr Lys Glu Ser Gln Glu Ile
 195 200 205
 Cys Phe Val Glu Lys Ser Tyr Ile Asp Thr Leu Lys Lys His Val Glu
 210 215 220
 Val Glu Lys Glu Gly Val Val Lys Asn Leu Gln Gly Glu Val Ile Gly
 225 230 235 240

aaa ggc gtc ttg cag agc gct cct ggc tat tca tat act aaa aat ggc 565
 Lys Gly Val Leu Gln Ser Ala Pro Gly Tyr Ser Tyr Thr Lys Asn Gly
 110 115 120 125
 tat gat ttc aaa aac aac cgc ccc ttt ttc ctg gcc ttt gaa gtc aaa 613
 Tyr Asp Phe Lys Asn Asn Arg Pro Phe Phe Leu Ala Phe Glu Val Lys
 130 135 140
 cct gat ggc aaa acc att ctt cct agc gtg gaa tta agc ctg att aaa 661
 Pro Asp Gly Lys Thr Ile Leu Pro Ser Val Glu Leu Ser Leu Ile Lys
 145 150 155
 acc cct aga ggc ttt tta ggg gtg ttc ttg ttt gat aat aat gaa aag 709
 Thr Pro Arg Gly Phe Leu Gly Val Phe Leu Phe Asp Asn Asn Glu Lys
 160 165 170
 ggg act aac gcc aag tgg att gag ggg agt ttg aat tta aag ctt aaa 757
 Gly Thr Asn Ala Lys Trp Ile Glu Gly Ser Leu Asn Leu Lys Leu Lys
 175 180 185
 aac gct tcc ttt aaa gat gcg tgg ggg ttg gaa caa taaagcatga 803
 Asn Ala Ser Phe Lys Asp Ala Trp Gly Leu Glu Gln
 190 195 200
 agtgatecgt tgcttttcgt aagctcttta tgattagatt gtaaaaaaat gccttgagta 863
 ttttttagat tttattaccc ctattcaatt ggaacaaagc cattaatatt ttaaaaactt 923
 ttaaaaacga taaacataat ccgcgctcca agtaacatag ctttcaaaaa tg 975

<210> 50
 <211> 201
 <212> PRT
 <213> Helicobacter pylori

<400> 50
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 1 5 10 15
 Gly His His Ser Gly Leu Val Asn Leu Tyr Ile Ala His Gln Gly Gln
 20 25 30
 Ser Val Arg Thr Tyr Trp Arg Lys Val Asp Arg Gly Val Ile Ala Lys
 35 40 45
 His Asn Glu Ala Leu Lys Lys Asp Pro Lys Ala Lys Leu Lys Asp Pro
 50 55 60
 Arg Gly Pro Leu Phe Met Leu Gly Ser Glu Arg Phe Met Leu Leu Trp
 65 70 75 80
 Lys Asn Arg Tyr Ala Leu Ala Lys Pro Gln Ser Phe Arg Leu Glu Pro
 85 90 95
 Gly Phe Tyr Tyr Leu Asp Ser Phe Ser Val Glu Thr Gln Lys Gly Val
 100 105 110
 Leu Gln Ser Ala Pro Gly Tyr Ser Tyr Thr Lys Asn Gly Tyr Asp Phe
 115 120 125
 Lys Asn Asn Arg Pro Phe Phe Leu Ala Phe Glu Val Lys Pro Asp Gly
 130 135 140
 Lys Thr Ile Leu Pro Ser Val Glu Leu Ser Leu Ile Lys Thr Pro Arg
 145 150 155 160
 Gly Phe Leu Gly Val Phe Leu Phe Asp Asn Asn Glu Lys Gly Thr Asn
 165 170 175
 Ala Lys Trp Ile Glu Gly Ser Leu Asn Leu Lys Leu Lys Asn Ala Ser

180 185 190
 Phe Lys Asp Ala Trp Gly Leu Glu Gln
 195 200

<210> 51
 <211> 1116
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (90)...(1076)

<400> 51
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 tatgaatttg tttattaagg gaaaaaatc atg tca aat agc atg ttg gat aaa 113
 Met Ser Asn Ser Met Leu Asp Lys
 1 5

 aat aaa gcg att ctt aca ggg ggt ggg gct tta tta tta ggg cta atc 161
 Asn Lys Ala Ile Leu Thr Gly Gly Gly Ala Leu Leu Leu Gly Leu Ile
 10 15 20

 gtg ctt ttt tat tta gct tat cgc cct aag gct gaa gtg ttg caa ggg 209
 Val Leu Phe Tyr Leu Ala Tyr Arg Pro Lys Ala Glu Val Leu Gln Gly
 25 30 35 40

 ttt ttg gaa gcc aga gaa tac agc gtg agc tcc aaa gtc cct ggc cgc 257
 Phe Leu Glu Ala Arg Glu Tyr Ser Val Ser Ser Lys Val Pro Gly Arg
 45 50 55

 att gaa aag gtg ttt gtt aaa aaa ggc gat cac att aaa aag ggc gat 305
 Ile Glu Lys Val Phe Val Lys Lys Gly Asp His Ile Lys Lys Gly Asp
 60 65 70

 ttg gtt ttt agc att tct agc cct gaa tta gaa gcc aaa ctc gct caa 353
 Leu Val Phe Ser Ile Ser Ser Pro Glu Leu Glu Ala Lys Leu Ala Gln
 75 80 85

 gct gaa gcc ggg cat aaa gcc gct aaa gcg ctt agc gat gaa gtc aaa 401
 Ala Glu Ala Gly His Lys Ala Ala Lys Ala Leu Ser Asp Glu Val Lys
 90 95 100

 aga ggc tca aga gac gaa acg att aat tct gcg aga gac gtt tgg caa 449
 Arg Gly Ser Arg Asp Glu Thr Ile Asn Ser Ala Arg Asp Val Trp Gln
 105 110 115 120

 gca gcc aaa tcc caa gcc act tta gcc aaa gag act tat aag cgc gtt 497
 Ala Ala Lys Ser Gln Ala Thr Leu Ala Lys Glu Thr Tyr Lys Arg Val
 125 130 135

 caa gat ttg tat gat aat ggc gtg gcg agc ttg caa aag cgc gat gaa 545
 Gln Asp Leu Tyr Asp Asn Gly Val Ala Ser Leu Gln Lys Arg Asp Glu
 140 145 150

 gcc tat gcg gct tat gaa agc act aaa tac aac gag agc gcg gct tac 593
 Ala Tyr Ala Ala Tyr Glu Ser Thr Lys Tyr Asn Glu Ser Ala Ala Tyr

155	160	165	
caa aag tat aaa atg gct tta ggg ggg gcg agc tct gaa agt aag att Gln Lys Tyr Lys Met Ala Leu Gly Gly Ala Ser Ser Glu Ser Lys Ile 170 175 180			641
gcc gct aag gct aaa gag agc gcg gct tta ggg caa gtg aat gaa gtg Ala Ala Lys Ala Lys Glu Ser Ala Ala Leu Gly Gln Val Asn Glu Val 185 190 195 200			689
gag tct tat tta aaa gac gtc aaa gcg aca gcc cca att gat ggg gaa Glu Ser Tyr Leu Lys Asp Val Lys Ala Thr Ala Pro Ile Asp Gly Glu 205 210 215			737
gtg agt aac gtg ctt tta agc ggt ggc gag ctt agc cct aag ggt ttt Val Ser Asn Val Leu Leu Ser Gly Gly Glu Leu Ser Pro Lys Gly Phe 220 225 230			785
cct gtg gtt tta atg ata gat tta aag gat agt tgg tta aaa atc agc Pro Val Val Leu Met Ile Asp Leu Lys Asp Ser Trp Leu Lys Ile Ser 235 240 245			833
gtg cct gaa aag tat ttg aac gag ttt aaa gtg ggt aag gaa ttt gaa Val Pro Glu Lys Tyr Leu Asn Glu Phe Lys Val Gly Lys Glu Phe Glu 250 255 260			881
ggc tat atc ccg gcg ttg aaa aaa agc acg aaa ttc agg gtc aaa tat Gly Tyr Ile Pro Ala Leu Lys Lys Ser Thr Lys Phe Arg Val Lys Tyr 265 270 275 280			929
ttg agc gtg atg ggg gat ttt gcg act tgg aaa gcg acg aat aat tcc Leu Ser Val Met Gly Asp Phe Ala Thr Trp Lys Ala Thr Asn Asn Ser 285 290 295			977
aac act tac gac atg aaa agc tat gaa gtg gaa gcc ata ccc tta gaa Asn Thr Tyr Asp Met Lys Ser Tyr Glu Val Glu Ala Ile Pro Leu Glu 300 305 310			1025
gag ttg gaa aat ttt agg gta ggg atg agc gtg tta gtt acc att aaa Glu Leu Glu Asn Phe Arg Val Gly Met Ser Val Leu Val Thr Ile Lys 315 320 325			1073
cct taaaaaggat tgttttgttc agattgataa gcgcattgggt Pro			1116

<210> 52

<211> 329

<212> PRT

<213> Helicobacter pylori

<400> 52

Met	Ser	Asn	Ser	Met	Leu	Asp	Lys	Asn	Lys	Ala	Ile	Leu	Thr	Gly	Gly
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Gly	Ala	Leu	Leu	Leu	Gly	Leu	Ile	Val	Leu	Phe	Tyr	Leu	Ala	Tyr	Arg
		20				25						30			
Pro	Lys	Ala	Glu	Val	Leu	Gln	Gly	Phe	Leu	Glu	Ala	Arg	Glu	Tyr	Ser

tct tta gcg tta tta atc acg ccc ttt gtt cgc att gat ggg gcg cat	210
Ser Leu Ala Leu Leu Ile Thr Pro Phe Val Arg Ile Asp Gly Ala His	
25 30 35	
ttg ttt ttg atc tct ttt gag cat aag caa ctg cat ttt tta ggc aag	258
Leu Phe Leu Ile Ser Phe Glu His Lys Gln Leu His Phe Leu Gly Lys	
40 45 50 55	
atc ttt agc gct gaa gaa ttg caa gtc atg cct ttt atg gtt att ttg	306
Ile Phe Ser Ala Glu Glu Leu Gln Val Met Pro Phe Met Val Ile Leu	
60 65 70	
ctt ttt ata ggg att ttt ttc atc acc act agc ctt ggg cgt gtg tgg	354
Leu Phe Ile Gly Ile Phe Phe Ile Thr Ser Leu Gly Arg Val Trp	
75 80 85	
tgc ggt tgg gct tgc ccg caa acc ttt tta agg gtg ctt tat aga gat	402
Cys Gly Trp Ala Cys Pro Gln Thr Phe Leu Arg Val Leu Tyr Arg Asp	
90 95 100	
gtg att gaa acc aag att ttc aaa ctc cat aaa aag atc agc aac aag	450
Val Ile Glu Thr Lys Ile Phe Lys Leu His Lys Lys Ile Ser Asn Lys	
105 110 115	
caa gaa agc cct aaa aac acc cca agc tac aag atc cgt aaa gta ttg	498
Gln Glu Ser Pro Lys Asn Thr Pro Ser Tyr Lys Ile Arg Lys Val Leu	
120 125 130 135	
agc gtt tta ttg ttc gct cct gtt gtg gcg ggg cta atg atg ttg ttt	546
Ser Val Leu Leu Phe Ala Pro Val Val Ala Gly Leu Met Met Leu Phe	
140 145 150	
ttc ttt tat ttc atc gcc cca gaa gat ttt ttt atg tat ctt aaa aac	594
Phe Phe Tyr Phe Ile Ala Pro Glu Asp Phe Phe Met Tyr Leu Lys Asn	
155 160 165	
cct agc gat cac cct att gct atg ggt ttt tgg ctt ttt agc acg gct	642
Pro Ser Asp His Pro Ile Ala Met Gly Phe Trp Leu Phe Ser Thr Ala	
170 175 180	
gtg gtg cta ttt gat ata gtg gtg gtt gcg gag cgt ttt tgc att tat	690
Val Val Leu Phe Asp Ile Val Val Val Ala Glu Arg Phe Cys Ile Tyr	
185 190 195	
tta tgc cct tac gct agg gtg caa tcg gtg ttg tat gac aat gac acc	738
Leu Cys Pro Tyr Ala Arg Val Gln Ser Val Leu Tyr Asp Asn Asp Thr	
200 205 210 215	
tta aac cct att tat gat gaa aag cgc ggc gga gcg ctt tat aat aat	786
Leu Asn Pro Ile Tyr Asp Glu Lys Arg Gly Gly Ala Leu Tyr Asn Asn	
220 225 230	
cag ggc cat ctc ttc ccc tta cct ccc aaa aaa cgc agc cca gaa aac	834
Gln Gly His Leu Phe Pro Leu Pro Pro Lys Lys Arg Ser Pro Glu Asn	
235 240 245	
gaa tgc gtg aat tgt ttg cat tgc gtg cag gtt tgc ccc acg cat att	882
Glu Cys Val Asn Cys Leu His Cys Val Gln Val Cys Pro Thr His Ile	

250	255	260	
gac atc agg aag ggc ttg caa tta gaa tgc atc aat tgt tta gaa tgc			930
Asp Ile Arg Lys Gly Leu Gln Leu Glu Cys Ile Asn Cys Leu Glu Cys			
265	270	275	
gtg gat gca tgc acg att acc atg gct aaa ttt aac cgc cct tca ctc			978
Val Asp Ala Cys Thr Ile Thr Met Ala Lys Phe Asn Arg Pro Ser Leu			
280	285	290	295
atc caa tgg tct tca act aac gct att aat acg cgc caa aaa gtg cac			1026
Ile Gln Trp Ser Ser Thr Asn Ala Ile Asn Thr Arg Gln Lys Val His			
	300	305	310
ctg gtg cgt tta aaa acg atc gct tac atg ggg gtt atc gct att gtg			1074
Leu Val Arg Leu Lys Thr Ile Ala Tyr Met Gly Val Ile Ala Ile Val			
	315	320	325
atc gct ctt tta gcc atc act tcg ttt aaa aaa gaa cgc atg ctc tta			1122
Ile Ala Leu Leu Ala Ile Thr Ser Phe Lys Lys Glu Arg Met Leu Leu			
	330	335	340
gac att aac cgc aac agc gat ctg tat gaa ttg cgc tct agc ggg tat			1170
Asp Ile Asn Arg Asn Ser Asp Leu Tyr Glu Leu Arg Ser Ser Gly Tyr			
	345	350	355
gtg gat aac gat tac gtg ttt tta ttc cac aac acg gac aat aaa gac			1218
Val Asp Asn Asp Tyr Val Phe Leu Phe His Asn Thr Asp Asn Lys Asp			
360	365	370	375
cat gag ttt tat ttc aaa gtt tta ggg caa aaa gac att cag atc aaa			1266
His Glu Phe Tyr Phe Lys Val Leu Gly Gln Lys Asp Ile Gln Ile Lys			
	380	385	390
aag cct tta aat cct atc gcc att aaa gcc ggg caa aag att aaa gcg			1314
Lys Pro Leu Asn Pro Ile Ala Ile Lys Ala Gly Gln Lys Ile Lys Ala			
	395	400	405
gta gtg att tta aga aaa ccc cta aag agt aac gcc aca gaa tac aag			1362
Val Val Ile Leu Arg Lys Pro Leu Lys Ser Asn Ala Thr Glu Tyr Lys			
	410	415	420
aac gct aaa gac gct cta atc ccc att acc ata caa gct tat agc gcg			1410
Asn Ala Lys Asp Ala Leu Ile Pro Ile Thr Ile Gln Ala Tyr Ser Ala			
	425	430	435
gac gat aag aat att acg ata gaa agg gaa tcg gtg ttt att gca cca			1458
Asp Asp Lys Asn Ile Thr Ile Glu Arg Glu Ser Val Phe Ile Ala Pro			
440	445	450	455
agt gag gat tgaagcctaa aactagcggt caatcacttc ataaggcaag			1507
Ser Glu Asp			
ccttggt			1514
<210> 54			
<211> 458			

<212> PRT
 <213> Helicobacter pylori

<400> 54

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Tyr	Ile	Gly	Phe	Leu	Leu	Ile	Ser	Leu	Ala	Leu	Leu	Ile	Thr	Pro	Phe
		20						25					30		
Val	Arg	Ile	Asp	Gly	Ala	His	Leu	Phe	Leu	Ile	Ser	Phe	Glu	His	Lys
		35					40					45			
Gln	Leu	His	Phe	Leu	Gly	Lys	Ile	Phe	Ser	Ala	Glu	Glu	Leu	Gln	Val
	50					55				60					
Met	Pro	Phe	Met	Val	Ile	Leu	Leu	Phe	Ile	Gly	Ile	Phe	Phe	Ile	Thr
65				70					75						80
Thr	Ser	Leu	Gly	Arg	Val	Trp	Cys	Gly	Trp	Ala	Cys	Pro	Gln	Thr	Phe
			85					90					95		
Leu	Arg	Val	Leu	Tyr	Arg	Asp	Val	Ile	Glu	Thr	Lys	Ile	Phe	Lys	Leu
		100					105						110		
His	Lys	Lys	Ile	Ser	Asn	Lys	Gln	Glu	Ser	Pro	Lys	Asn	Thr	Pro	Ser
	115						120					125			
Tyr	Lys	Ile	Arg	Lys	Val	Leu	Ser	Val	Leu	Leu	Phe	Ala	Pro	Val	Val
	130					135					140				
Ala	Gly	Leu	Met	Met	Leu	Phe	Phe	Phe	Tyr	Phe	Ile	Ala	Pro	Glu	Asp
145				150					155						160
Phe	Phe	Met	Tyr	Leu	Lys	Asn	Pro	Ser	Asp	His	Pro	Ile	Ala	Met	Gly
			165					170					175		
Phe	Trp	Leu	Phe	Ser	Thr	Ala	Val	Val	Leu	Phe	Asp	Ile	Val	Val	Val
		180					185						190		
Ala	Glu	Arg	Phe	Cys	Ile	Tyr	Leu	Cys	Pro	Tyr	Ala	Arg	Val	Gln	Ser
	195						200					205			
Val	Leu	Tyr	Asp	Asn	Asp	Thr	Leu	Asn	Pro	Ile	Tyr	Asp	Glu	Lys	Arg
	210					215					220				
Gly	Gly	Ala	Leu	Tyr	Asn	Asn	Gln	Gly	His	Leu	Phe	Pro	Leu	Pro	Pro
225				230					235						240
Lys	Lys	Arg	Ser	Pro	Glu	Asn	Glu	Cys	Val	Asn	Cys	Leu	His	Cys	Val
			245					250					255		
Gln	Val	Cys	Pro	Thr	His	Ile	Asp	Ile	Arg	Lys	Gly	Leu	Gln	Leu	Glu
		260					265						270		
Cys	Ile	Asn	Cys	Leu	Glu	Cys	Val	Asp	Ala	Cys	Thr	Ile	Thr	Met	Ala
	275						280					285			
Lys	Phe	Asn	Arg	Pro	Ser	Leu	Ile	Gln	Trp	Ser	Ser	Thr	Asn	Ala	Ile
	290					295					300				
Asn	Thr	Arg	Gln	Lys	Val	His	Leu	Val	Arg	Leu	Lys	Thr	Ile	Ala	Tyr
305				310					315						320
Met	Gly	Val	Ile	Ala	Ile	Val	Ile	Ala	Leu	Leu	Ala	Ile	Thr	Ser	Phe
			325					330					335		
Lys	Lys	Glu	Arg	Met	Leu	Leu	Asp	Ile	Asn	Arg	Asn	Ser	Asp	Leu	Tyr
		340					345					350			
Glu	Leu	Arg	Ser	Ser	Gly	Tyr	Val	Asp	Asn	Asp	Tyr	Val	Phe	Leu	Phe
	355						360					365			
His	Asn	Thr	Asp	Asn	Lys	Asp	His	Glu	Phe	Tyr	Phe	Lys	Val	Leu	Gly
	370					375					380				
Gln	Lys	Asp	Ile	Gln	Ile	Lys	Lys	Pro	Leu	Asn	Pro	Ile	Ala	Ile	Lys
385				390					395						400
Ala	Gly	Gln	Lys	Ile	Lys	Ala	Val	Val	Ile	Leu	Arg	Lys	Pro	Leu	Lys
			405					410					415		
Ser	Asn	Ala	Thr	Glu	Tyr	Lys	Asn	Ala	Lys	Asp	Ala	Leu	Ile	Pro	Ile
			420				425						430		

Thr Ile Gln Ala Tyr Ser Ala Asp Asp Lys Asn Ile Thr Ile Glu Arg
 435 440 445
 Glu Ser Val Phe Ile Ala Pro Ser Glu Asp
 450 455

<210> 55
 <211> 990
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (228)...(782)

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 cttcgcaaaa aagaacgaac aacgttttgc aacgagccac taaccaccaa gacaatctca 120
 attccccact caacaggaag tattaaagtg tgaaactttt ttcaaaggat ttattttaaaa 180
 aagtaacccc tttattttta agcgtttatt ttttaaaccc caccatt atg caa gcc 236
 Met Gln Ala
 1
 aaa agc cgt ttt tat gtg gct tct caa tac cag gtg ggg aaa atg atc 284
 Lys Ser Arg Phe Tyr Val Ala Ser Gln Tyr Gln Val Gly Lys Met Ile
 5 10 15
 atg aaa aaa tac aac gat ctc aaa cgc acg att gaa ggg gcg agc ttt 332
 Met Lys Lys Tyr Asn Asp Leu Lys Arg Thr Ile Glu Gly Ala Ser Phe
 20 25 30 35
 tct tta ggc tgg gag att aac ccc act aac tac tgg ttt tat tcg cgc 380
 Ser Leu Gly Trp Glu Ile Asn Pro Thr Asn Tyr Trp Phe Tyr Ser Arg
 40 45 50
 tat tac ttt ttt atg gat tac ggg aat gtc att ctc aat aaa aga acg 428
 Tyr Tyr Phe Phe Met Asp Tyr Gly Asn Val Ile Leu Asn Lys Arg Thr
 55 60 65
 ggc gct caa gcg aac atg ttc act tat ggc ttt ggg ggg gat ttg att 476
 Gly Ala Gln Ala Asn Met Phe Thr Tyr Gly Phe Gly Gly Asp Leu Ile
 70 75 80
 gtg gaa tac aat aaa aac ccc ttg tat gta ttt tct ctt ttt tat ggc 524
 Val Glu Tyr Asn Lys Asn Pro Leu Tyr Val Phe Ser Leu Phe Tyr Gly
 85 90 95
 atg caa gtt gct gaa aac aca tgg acg att tcc aaa cac agc gcg aat 572
 Met Gln Val Ala Glu Asn Thr Trp Thr Ile Ser Lys His Ser Ala Asn
 100 105 110 115
 ttc atc att gac gat tgg cgc agc att caa ggg ttt tcg ctc aaa act 620
 Phe Ile Ile Asp Asp Trp Arg Ser Ile Gln Gly Phe Ser Leu Lys Thr
 120 125 130
 tcc aat ttt agg atg ttg ggt tta gtg ggg ttt aaa ttc caa acc gtg 668
 Ser Asn Phe Arg Met Leu Gly Leu Val Gly Phe Lys Phe Gln Thr Val
 135 140 145

cta ttc cac cat gac gca agt att gaa gtg ggg atc aaa tgg cct ttt 716
 Leu Phe His His Asp Ala Ser Ile Glu Val Gly Ile Lys Trp Pro Phe
 150 155 160

gct ttt gaa tac gac tca gcc ttt gta agg ctt ttt tct gtc ttt att 764
 Ala Phe Glu Tyr Asp Ser Ala Phe Val Arg Leu Phe Ser Val Phe Ile
 165 170 175

tcg cac act ttc tac ctt taaactaatt ccaaccctac cgggcaatga 812
 Ser His Thr Phe Tyr Leu
 180 185

tcgctcccta aaatatcttt atagattaaa gcgtctttta agcgcggtttt taaagggtta 872
 gagcataaaa aataatcaat gcgccaacca atgtttttat cccttgcttg ttgcatgtaa 932
 ctccaccagg tgtaagcctt ttctttgtta gggtaaaaaat aacggaaagt gtcaataa 990

<210> 56
 <211> 185
 <212> PRT
 <213> Helicobacter pylori

<400> 56
 Met Gln Ala Lys Ser Arg Phe Tyr Val Ala Ser Gln Tyr Gln Val Gly
 1 5 10 15
 Lys Met Ile Met Lys Lys Tyr Asn Asp Leu Lys Arg Thr Ile Glu Gly
 20 25 30
 Ala Ser Phe Ser Leu Gly Trp Glu Ile Asn Pro Thr Asn Tyr Trp Phe
 35 40 45
 Tyr Ser Arg Tyr Tyr Phe Phe Met Asp Tyr Gly Asn Val Ile Leu Asn
 50 55 60
 Lys Arg Thr Gly Ala Gln Ala Asn Met Phe Thr Tyr Gly Phe Gly Gly
 65 70 75 80
 Asp Leu Ile Val Glu Tyr Asn Lys Asn Pro Leu Tyr Val Phe Ser Leu
 85 90 95
 Phe Tyr Gly Met Gln Val Ala Glu Asn Thr Trp Thr Ile Ser Lys His
 100 105 110
 Ser Ala Asn Phe Ile Ile Asp Asp Trp Arg Ser Ile Gln Gly Phe Ser
 115 120 125
 Leu Lys Thr Ser Asn Phe Arg Met Leu Gly Leu Val Gly Phe Lys Phe
 130 135 140
 Gln Thr Val Leu Phe His His Asp Ala Ser Ile Glu Val Gly Ile Lys
 145 150 155 160
 Trp Pro Phe Ala Phe Glu Tyr Asp Ser Ala Phe Val Arg Leu Phe Ser
 165 170 175
 Val Phe Ile Ser His Thr Phe Tyr Leu
 180 185

<210> 57
 <211> 1161
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (109)...(1113)

<400> 57

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tcttagtaat	gttataatcg	ctttataaat	catacaaaaa	ggatcgct	atg tta gtt	117
					Met Leu Val	
					1	
act cgc ttt aaa aaa gct ttc att tct tat tct tta ggc gtg ctt gtc	165					
Thr Arg Phe Lys Lys Ala Phe Ile Ser Tyr Ser Leu Gly Val Leu Val						
5 10 15						
gct tca tta tgg ttg aac gtg tgc aac gct tca gcg caa gaa gtc aaa	213					
Ala Ser Leu Trp Leu Asn Val Cys Asn Ala Ser Ala Gln Glu Val Lys						
20 25 30 35						
gtc aag gat tat ttc ggg gag caa acc atc aag ctt cct gtt tct aaa	261					
Val Lys Asp Tyr Phe Gly Glu Gln Thr Ile Lys Leu Pro Val Ser Lys						
40 45 50						
ata gcc tat ata ggg agc tat gta gaa gtg cct gcc atg ctt aat gtt	309					
Ile Ala Tyr Ile Gly Ser Tyr Val Glu Val Pro Ala Met Leu Asn Val						
55 60 65						
tgg aat agg gtt gta ggc gtt tcg gat tac gct ttt aaa gac gat att	357					
Trp Asn Arg Val Val Gly Val Ser Asp Tyr Ala Phe Lys Asp Asp Ile						
70 75 80						
gtc aaa gcc act ctc aaa ggc gaa gat ctt aaa cgc gtc aaa cac atg	405					
Val Lys Ala Thr Leu Lys Gly Glu Asp Leu Lys Arg Val Lys His Met						
85 90 95						
agc act gat cat aca gcc gcg cta aat gta gag ctt tta aaa aag ctt	453					
Ser Thr Asp His Thr Ala Ala Leu Asn Val Glu Leu Leu Lys Lys Leu						
100 105 110 115						
agc cct gat ctt gtg gta acc ttt gtg ggc aac cct aaa gcg gta gag	501					
Ser Pro Asp Leu Val Val Thr Phe Val Gly Asn Pro Lys Ala Val Glu						
120 125 130						
cat gcg aaa aaa ttt ggt ata tca ttt ctt tct ttt caa gag aca acg	549					
His Ala Lys Lys Phe Gly Ile Ser Phe Leu Ser Phe Gln Glu Thr Thr						
135 140 145						
att gca gag gcc atg cag gcc atg caa gct caa gcc acg gtt tta gag	597					
Ile Ala Glu Ala Met Gln Ala Met Gln Ala Gln Ala Thr Val Leu Glu						
150 155 160						
att gac gct tcc aaa aaa ttc gcc aaa atg caa gaa act ttg gat ttt	645					
Ile Asp Ala Ser Lys Lys Phe Ala Lys Met Gln Glu Thr Leu Asp Phe						
165 170 175						
att gct gag cgt ttg aaa aat gtc aaa aag aaa aag ggg gtg gag ctt	693					
Ile Ala Glu Arg Leu Lys Asn Val Lys Lys Lys Lys Gly Val Glu Leu						
180 185 190 195						
ttc cat aaa gcc aat aaa atc agc ggc cat caa gcc att agc tca gac	741					
Phe His Lys Ala Asn Lys Ile Ser Gly His Gln Ala Ile Ser Ser Asp						
200 205 210						

att tta gaa aaa ggg ggc ata gac aat ttt ggc ttg aaa tat gtc aaa	789
Ile Leu Glu Lys Gly Gly Ile Asp Asn Phe Gly Leu Lys Tyr Val Lys	
215 220 225	
ttt ggg cgt gct gac att agc gtg gaa aaa atc gtt aaa gaa aac cct	837
Phe Gly Arg Ala Asp Ile Ser Val Glu Lys Ile Val Lys Glu Asn Pro	
230 235 240	
gag att atc ttt att tgg tgg ata agc cca ctc acg cct gaa gat gtg	885
Glu Ile Ile Phe Ile Trp Trp Ile Ser Pro Leu Thr Pro Glu Asp Val	
245 250 255	
tta aac aac ccc aaa ttt gct acc atc aaa gcc att aaa aac aag cag	933
Leu Asn Asn Pro Lys Phe Ala Thr Ile Lys Ala Ile Lys Asn Lys Gln	
260 265 270 275	
gtt tat aaa ctc ccc aca atg gat att ggc ggg cct aga gcc cca ctc	981
Val Tyr Lys Leu Pro Thr Met Asp Ile Gly Gly Pro Arg Ala Pro Leu	
280 285 290	
ata agt ctt ttt atc gct cta aaa gcc cac cct gaa gcc ttt aag ggc	1029
Ile Ser Leu Phe Ile Ala Leu Lys Ala His Pro Glu Ala Phe Lys Gly	
295 300 305	
gtg gat att aat gcg atg gtt aaa gac tac tat aaa gtg gtt ttt gat	1077
Val Asp Ile Asn Ala Met Val Lys Asp Tyr Tyr Lys Val Val Phe Asp	
310 315 320	
ttg aat gat gca gag gtt gag ccc ttt tta tgg cat taatttttaa	1123
Leu Asn Asp Ala Glu Val Glu Pro Phe Leu Trp His	
325 330 335	
aaaggggttg atgttttttag cctttcgtgt atcgcgct	1161
<210> 58	
<211> 335	
<212> PRT	
<213> Helicobacter pylori	
<400> 58	
Met Leu Val Thr Arg Phe Lys Lys Ala Phe Ile Ser Tyr Ser Leu Gly	
1 5 10 15	
Val Leu Val Ala Ser Leu Trp Leu Asn Val Cys Asn Ala Ser Ala Gln	
20 25 30	
Glu Val Lys Val Lys Asp Tyr Phe Gly Glu Gln Thr Ile Lys Leu Pro	
35 40 45	
Val Ser Lys Ile Ala Tyr Ile Gly Ser Tyr Val Glu Val Pro Ala Met	
50 55 60	
Leu Asn Val Trp Asn Arg Val Val Gly Val Ser Asp Tyr Ala Phe Lys	
65 70 75 80	
Asp Asp Ile Val Lys Ala Thr Leu Lys Gly Glu Asp Leu Lys Arg Val	
85 90 95	
Lys His Met Ser Thr Asp His Thr Ala Ala Leu Asn Val Glu Leu Leu	
100 105 110	
Lys Lys Leu Ser Pro Asp Leu Val Val Thr Phe Val Gly Asn Pro Lys	
115 120 125	
Ala Val Glu His Ala Lys Lys Phe Gly Ile Ser Phe Leu Ser Phe Gln	
130 135 140	

Glu	Thr	Thr	Ile	Ala	Glu	Ala	Met	Gln	Ala	Met	Gln	Ala	Gln	Ala	Thr
145					150					155					160
Val	Leu	Glu	Ile	Asp	Ala	Ser	Lys	Lys	Phe	Ala	Lys	Met	Gln	Glu	Thr
				165					170						175
Leu	Asp	Phe	Ile	Ala	Glu	Arg	Leu	Lys	Asn	Val	Lys	Lys	Lys	Lys	Gly
			180					185					190		
Val	Glu	Leu	Phe	His	Lys	Ala	Asn	Lys	Ile	Ser	Gly	His	Gln	Ala	Ile
		195					200					205			
Ser	Ser	Asp	Ile	Leu	Glu	Lys	Gly	Gly	Ile	Asp	Asn	Phe	Gly	Leu	Lys
	210					215					220				
Tyr	Val	Lys	Phe	Gly	Arg	Ala	Asp	Ile	Ser	Val	Glu	Lys	Ile	Val	Lys
225					230					235					240
Glu	Asn	Pro	Glu	Ile	Phe	Ile	Trp	Trp	Ile	Ser	Pro	Leu	Thr	Pro	
			245					250					255		
Glu	Asp	Val	Leu	Asn	Asn	Pro	Lys	Phe	Ala	Thr	Ile	Lys	Ala	Ile	Lys
		260						265					270		
Asn	Lys	Gln	Val	Tyr	Lys	Leu	Pro	Thr	Met	Asp	Ile	Gly	Gly	Pro	Arg
	275						280					285			
Ala	Pro	Leu	Ile	Ser	Leu	Phe	Ile	Ala	Leu	Lys	Ala	His	Pro	Glu	Ala
	290					295					300				
Phe	Lys	Gly	Val	Asp	Ile	Asn	Ala	Met	Val	Lys	Asp	Tyr	Tyr	Lys	Val
305					310					315					320
Val	Phe	Asp	Leu	Asn	Asp	Ala	Glu	Val	Glu	Pro	Phe	Leu	Trp	His	
			325						330					335	

<210> 59
 <211> 800
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (121)...(669)

<400> 59
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 tgaaatcaaaa caaagccaaa aagaaaagaa aaaattcccc actttcaaag gaggttttta 120
 atg cgt tgg tgg tgt ttt ttg gtg tgt tgt ttt ggt att tta agc gtg 168
 Met Arg Trp Trp Cys Phe Leu Val Cys Cys Phe Gly Ile Leu Ser Val
 1 5 10 15

 atg gac gct aaa aaa tta gag aat aag aat ttg aaa aaa gaa aga gag 216
 Met Asp Ala Lys Lys Leu Glu Asn Lys Asn Leu Lys Lys Glu Arg Glu
 20 25 30

 ctt tta gag att act ggc aac caa ttt gta gcg aac gac aaa acc aaa 264
 Leu Leu Glu Ile Thr Gly Asn Gln Phe Val Ala Asn Asp Lys Thr Lys
 35 40 45

 acc gct gtt att caa ggc aat gtg cag atc aaa aag ggt aaa gac cgg 312
 Thr Ala Val Ile Gln Gly Asn Val Gln Ile Lys Lys Gly Lys Asp Arg
 50 55 60

 ttg ttt gcg gac aag gtg agc gtg ttt tta aac gat aaa cga aag cca 360
 Leu Phe Ala Asp Lys Val Ser Val Phe Leu Asn Asp Lys Arg Lys Pro
 65 70 75 80

gag cgc tat gaa gcc aca ggg aac acg cat ttt aac atc ttt aca gag 408
 Glu Arg Tyr Glu Ala Thr Gly Asn Thr His Phe Asn Ile Phe Thr Glu
 85 90 95
 gac aat cgt gaa atc agc ggg agt gct gac aag ctc att tat aac gcg 456
 Asp Asn Arg Glu Ile Ser Gly Ser Ala Asp Lys Leu Ile Tyr Asn Ala
 100 105 110
 ctg aat ggg gaa tac aaa tta ttg caa aat gcg gtg gtt aga gaa gtg 504
 Leu Asn Gly Glu Tyr Lys Leu Leu Gln Asn Ala Val Val Arg Glu Val
 115 120 125
 ggg aaa tcc aat gtc atc acc ggc gat gaa atc att tta aac aaa act 552
 Gly Lys Ser Asn Val Ile Thr Gly Asp Glu Ile Ile Leu Asn Lys Thr
 130 135 140
 aag ggt tat gct gat gtg ttg ggg agc gcg aaa cgg ccc gct aaa ttc 600
 Lys Gly Tyr Ala Asp Val Leu Gly Ser Ala Lys Arg Pro Ala Lys Phe
 145 150 155 160
 gtg ttt gat atg gaa gat att aat gaa gaa aat cgt aag gct aaa ttg 648
 Val Phe Asp Met Glu Asp Ile Asn Glu Glu Asn Arg Lys Ala Lys Leu
 165 170 175
 aag aag aaa ggc gaa aaa cca tgattgtcat taaagacgct cattttctca 699
 Lys Lys Lys Gly Glu Lys Pro
 180
 cttcttcaag ccaacttttt caatgccctg cgagtttgac ttctgaaatg gtgggttttag 759
 ggcgagcaaa tgtaggcaaa agctcggtta ttaatacctt g 800

<210> 60

<211> 183

<212> PRT

<213> Helicobacter pylori

<400> 60

Met Arg Trp Trp Cys Phe Leu Val Cys Cys Phe Gly Ile Leu Ser Val
 1 5 10 15
 Met Asp Ala Lys Lys Leu Glu Asn Lys Asn Leu Lys Lys Glu Arg Glu
 20 25 30
 Leu Leu Glu Ile Thr Gly Asn Gln Phe Val Ala Asn Asp Lys Thr Lys
 35 40 45
 Thr Ala Val Ile Gln Gly Asn Val Gln Ile Lys Lys Gly Lys Asp Arg
 50 55 60
 Leu Phe Ala Asp Lys Val Ser Val Phe Leu Asn Asp Lys Arg Lys Pro
 65 70 75 80
 Glu Arg Tyr Glu Ala Thr Gly Asn Thr His Phe Asn Ile Phe Thr Glu
 85 90 95
 Asp Asn Arg Glu Ile Ser Gly Ser Ala Asp Lys Leu Ile Tyr Asn Ala
 100 105 110
 Leu Asn Gly Glu Tyr Lys Leu Leu Gln Asn Ala Val Val Arg Glu Val
 115 120 125
 Gly Lys Ser Asn Val Ile Thr Gly Asp Glu Ile Ile Leu Asn Lys Thr
 130 135 140
 Lys Gly Tyr Ala Asp Val Leu Gly Ser Ala Lys Arg Pro Ala Lys Phe
 145 150 155 160
 Val Phe Asp Met Glu Asp Ile Asn Glu Glu Asn Arg Lys Ala Lys Leu

Lys Lys Lys Gly Glu Lys Pro
180

170

175

<210> 61
<211> 724
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (88)...(618)

<400> 61
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aaaaaaaggc taatactatc ataagga atg aag ttg ata aaa ttt gtg cgt aat 114
Met Lys Leu Ile Lys Phe Val Arg Asn
1 5

gtg gtt ttg ttc att tta acg gcg atc ttt tta gcg ttc atg ctt ttg 162
Val Val Leu Phe Ile Leu Thr Ala Ile Phe Leu Ala Phe Met Leu Leu
10 15 20 25

gtg agt tat tgc atg ccc cat tat agc gcg gct gtc att agc ggg gtg 210
Val Ser Tyr Cys Met Pro His Tyr Ser Ala Ala Val Ile Ser Gly Val
30 35 40

gaa gtc aaa aga atg aat gaa aat gaa aac acg ccc aat aat aag gaa 258
Glu Val Lys Arg Met Asn Glu Asn Glu Asn Thr Pro Asn Asn Lys Glu
45 50 55

gta aaa acc ctt gct aga gat gtc tat ttt gtg caa act tac gac cct 306
Val Lys Thr Leu Ala Arg Asp Val Tyr Phe Val Gln Thr Tyr Asp Pro
60 65 70

aaa gat caa aaa agc gta acc gtt tat cgt aac gaa gac acg cgc ttt 354
Lys Asp Gln Lys Ser Val Thr Val Tyr Arg Asn Glu Asp Thr Arg Phe
75 80 85

agc ttc cct ttt tat ttt aag ttt aat tcg gct gat att tca gcc ctc 402
Ser Phe Pro Phe Tyr Phe Lys Phe Asn Ser Ala Asp Ile Ser Ala Leu
90 95 100 105

gct caa agt tta atc aat cag caa gtg gaa gtg aaa tac tat ggt tgg 450
Ala Gln Ser Leu Ile Asn Gln Gln Val Glu Val Lys Tyr Tyr Gly Trp
110 115 120

cgg atc aat ttg ttt aac atg ttc cct aat gtg att ttt tta aag ccc 498
Arg Ile Asn Leu Phe Asn Met Phe Pro Asn Val Ile Phe Leu Lys Pro
125 130 135

tta aaa gag agc act gac att tca aag ccc att ttt agc tgg att tta 546
Leu Lys Glu Ser Thr Asp Ile Ser Lys Pro Ile Phe Ser Trp Ile Leu
140 145 150

tac gct ttg ctg tta atg ggc ttt ttt atc agc gcg cgt tct gtt tgc 594
Tyr Ala Leu Leu Leu Met Gly Phe Phe Ile Ser Ala Arg Ser Val Cys

155

160

165

act tta ttt aag agc aaa gct cat taaaactttt aggctttgtt ggaaaatcac 648
 Thr Leu Phe Lys Ser Lys Ala His
 170 175

aatgggggta ttggagcgtg tattaaaaag ctcaatatag ggcaagctga tgctgtgaaa 708
 agcgggtgtt tttcct 724

<210> 62

<211> 177

<212> PRT

<213> Helicobacter pylori

<400> 62

Met Lys Leu Ile Lys Phe Val Arg Asn Val Val Leu Phe Ile Leu Thr
 1 5 10 15
 Ala Ile Phe Leu Ala Phe Met Leu Leu Val Ser Tyr Cys Met Pro His
 20 25 30
 Tyr Ser Ala Ala Val Ile Ser Gly Val Glu Val Lys Arg Met Asn Glu
 35 40 45
 Asn Glu Asn Thr Pro Asn Asn Lys Glu Val Lys Thr Leu Ala Arg Asp
 50 55 60
 Val Tyr Phe Val Gln Thr Tyr Asp Pro Lys Asp Gln Lys Ser Val Thr
 65 70 75 80
 Val Tyr Arg Asn Glu Asp Thr Arg Phe Ser Phe Pro Phe Tyr Phe Lys
 85 90 95
 Phe Asn Ser Ala Asp Ile Ser Ala Leu Ala Gln Ser Leu Ile Asn Gln
 100 105 110
 Gln Val Glu Val Lys Tyr Tyr Gly Trp Arg Ile Asn Leu Phe Asn Met
 115 120 125
 Phe Pro Asn Val Ile Phe Leu Lys Pro Leu Lys Glu Ser Thr Asp Ile
 130 135 140
 Ser Lys Pro Ile Phe Ser Trp Ile Leu Tyr Ala Leu Leu Leu Met Gly
 145 150 155 160
 Phe Phe Ile Ser Ala Arg Ser Val Cys Thr Leu Phe Lys Ser Lys Ala
 165 170 175
 His

<210> 63

<211> 1041

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (162)...(896)

<400> 63

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 tttttgttat tatgggactt gtgttttttg gttgcaccag taagggtgcat gagatgaaaa 120
 aaagcccttg cacattgtta tgaaaacagg ttaaactctcg c atg aaa gaa aag cct 176
 Met Lys Glu Lys Pro
 1 5

ttc aat agc gag cag ttg atc tat tta gaa gag ctt tta aac cac caa 224

Phe	Asn	Ser	Glu	Gln	Leu	Ile	Tyr	Leu	Glu	Glu	Leu	Leu	Asn	His	Gln		
				10					15					20			
gaa	aag	cat	tta	gaa	aac	aag	ctt	tct	ggg	ttt	tcg	gtg	aat	gat	ttg	272	
Glu	Lys	His		Leu	Asn	Lys	Leu	Ser	Gly	Phe	Ser	Val	Asn	Asp	Leu		
			25				30						35				
gac	atg	caa	agc	gtg	ttc	aga	ctg	gag	agg	aac	cgc	ttg	aaa	atc	gct	320	
Asp	Met	Gln	Ser	Val	Phe	Arg	Leu	Glu	Arg	Asn	Arg	Leu	Lys	Ile	Ala		
		40					45					50					
tat	aaa	ctc	tta	ggc	ttg	atg	agt	ttt	atc	gct	ctt	gtt	tta	gcg	atc	368	
Tyr	Lys		Leu	Leu	Gly	Leu	Met	Ser	Phe	Ile	Ala	Leu	Val	Leu	Ala	Ile	
	55					60					65						
gtg	tta	atc	agt	gtt	ctg	ccc	tta	caa	aaa	acc	gaa	cac	cat	ttc	gtg	416	
Val	Leu	Ile	Ser	Val	Leu	Pro	Leu	Gln	Lys	Thr	Glu	His	His	Phe	Val		
	70				75					80					85		
gat	ttt	tta	aat	cag	gac	aag	cat	tac	gcc	att	atc	caa	aga	gcg	gat	464	
Asp	Phe	Leu	Asn	Gln	Asp	Lys	His	Tyr	Ala	Ile	Ile	Gln	Arg	Ala	Asp		
				90					95					100			
aaa	agc	att	tcc	agt	aat	gaa	gcg	ttg	gct	cgt	tcg	ctc	att	ggg	gcg	512	
Lys	Ser	Ile	Ser	Ser	Asn	Glu	Ala	Leu	Ala	Arg	Ser	Leu	Ile	Gly	Ala		
			105					110					115				
tat	gtg	tta	aac	cga	gag	agt	att	aac	cgc	att	gac	gat	aaa	tcg	cgc	560	
Tyr	Val	Leu	Asn	Arg	Glu	Ser	Ile	Asn	Arg	Ile	Asp	Asp	Lys	Ser	Arg		
		120					125					130					
tat	gaa	ttg	gtg	cgc	ttg	caa	agc	agt	tct	aaa	gtg	tgg	caa	cgc	ttt	608	
Tyr	Glu	Leu	Val	Arg	Leu	Gln	Ser	Ser	Ser	Lys	Val	Trp	Gln	Arg	Phe		
	135					140					145						
gaa	gat	ttg	att	aaa	acc	caa	aac	agc	att	tat	gtg	caa	agc	cat	ttg	656	
Glu	Asp	Leu	Ile	Lys	Thr	Gln	Asn	Ser	Ile	Tyr	Val	Gln	Ser	His	Leu		
	150				155				160						165		
gaa	aga	gaa	gtc	cat	atc	gtc	aat	att	gcg	atc	tat	cag	caa	gac	aat	704	
Glu	Arg	Glu	Val	His	Ile	Val	Asn	Ile	Ala	Ile	Tyr	Gln	Gln	Asp	Asn		
				170					175					180			
aac	ccc	att	gcg	agc	gtc	tcc	att	gcg	gct	aaa	ctt	ttg	aac	gaa	aac	752	
Asn	Pro	Ile	Ala	Ser	Val	Ser	Ile	Ala	Ala	Lys	Leu	Leu	Asn	Glu	Asn		
			185					190					195				
aag	ttg	gtg	tat	gaa	aag	cgt	tat	aaa	atc	gta	ttg	agt	tat	ttg	ttt	800	
Lys	Leu	Val	Tyr	Glu	Lys	Arg	Tyr	Lys	Ile	Val	Leu	Ser	Tyr	Leu	Phe		
		200					205					210					
gac	acc	ccg	gat	ttt	gat	tac	gct	tcc	atg	cct	aaa	aac	cct	acc	gga	848	
Asp	Thr	Pro	Asp	Phe	Asp	Tyr	Ala	Ser	Met	Pro	Lys	Asn	Pro	Thr	Gly		
	215					220					225						
ttt	aaa	atc	acc	cgt	tac	agc	atc	act	gaa	atc	act	aat	agg	ggg	gat	896	
Phe	Lys	Ile	Thr	Arg	Tyr	Ser	Ile	Thr	Glu	Ile	Thr	Asn	Arg	Gly	Asp		
					235					240					245		

tgatgcgtaa gggtttatac gctcttgtgg gctttttggt ggcttttagc gctttaaaag 956
 ccgatgattt tttagaagaa gcgaacgaaa cagccccggc gcatttaaac caccctatgc 1016
 aggatttaaa cgccattcaa gggag 1041

<210> 64
 <211> 245
 <212> PRT
 <213> Helicobacter pylori

<400> 64
 Met Lys Glu Lys Pro Phe Asn Ser Glu Gln Leu Ile Tyr Leu Glu Glu
 1 5 10 15
 Leu Leu Asn His Gln Glu Lys His Leu Glu Asn Lys Leu Ser Gly Phe
 20 25 30
 Ser Val Asn Asp Leu Asp Met Gln Ser Val Phe Arg Leu Glu Arg Asn
 35 40 45
 Arg Leu Lys Ile Ala Tyr Lys Leu Leu Gly Leu Met Ser Phe Ile Ala
 50 55 60
 Leu Val Leu Ala Ile Val Leu Ile Ser Val Leu Pro Leu Gln Lys Thr
 65 70 75 80
 Glu His His Phe Val Asp Phe Leu Asn Gln Asp Lys His Tyr Ala Ile
 85 90 95
 Ile Gln Arg Ala Asp Lys Ser Ile Ser Ser Asn Glu Ala Leu Ala Arg
 100 105 110
 Ser Leu Ile Gly Ala Tyr Val Leu Asn Arg Glu Ser Ile Asn Arg Ile
 115 120 125
 Asp Asp Lys Ser Arg Tyr Glu Leu Val Arg Leu Gln Ser Ser Ser Lys
 130 135 140
 Val Trp Gln Arg Phe Glu Asp Leu Ile Lys Thr Gln Asn Ser Ile Tyr
 145 150 155 160
 Val Gln Ser His Leu Glu Arg Glu Val His Ile Val Asn Ile Ala Ile
 165 170 175
 Tyr Gln Gln Asp Asn Asn Pro Ile Ala Ser Val Ser Ile Ala Ala Lys
 180 185 190
 Leu Leu Asn Glu Asn Lys Leu Val Tyr Glu Lys Arg Tyr Lys Ile Val
 195 200 205
 Leu Ser Tyr Leu Phe Asp Thr Pro Asp Phe Asp Tyr Ala Ser Met Pro
 210 215 220
 Lys Asn Pro Thr Gly Phe Lys Ile Thr Arg Tyr Ser Ile Thr Glu Ile
 225 230 235 240
 Thr Asn Arg Gly Asp
 245

<210> 65
 <211> 2059
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (183)...(1961)

<400> 65
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 cgcttaaaac agaacctttt gttttttagg ttttattttt tactttggct tgttttcaaa 120
 agtcattttg atttctaaaa atagtctata atgctcgcaa gagatatttt ttaagggttat 180

ca atg aaa gct ata aaa ata ctt ttt ata atg aca ctc agt tta aac	227
Met Lys Ala Ile Lys Ile Leu Phe Ile Met Thr Leu Ser Leu Asn	
1 5 10 15	
gct atc agc gtg aat agg gcg ttg ttt gat tta aaa gat tcg caa tta	275
Ala Ile Ser Val Asn Arg Ala Leu Phe Asp Leu Lys Asp Ser Gln Leu	
20 25 30	
aaa ggg gaa tta acg cca aaa ata gtg aat ttt ggg ggt tat aaa agc	323
Lys Gly Glu Leu Thr Pro Lys Ile Val Asn Phe Gly Gly Tyr Lys Ser	
35 40 45	
agc act gaa gag tgg ggg gct acg gct tta aac tat atc aat gcg gct	371
Ser Thr Glu Glu Trp Gly Ala Thr Ala Leu Asn Tyr Ile Asn Ala Ala	
50 55 60	
aat ggc gat gcg aaa aaa ttc agc act cta gtg gaa aaa atg cgt ttt	419
Asn Gly Asp Ala Lys Lys Phe Ser Thr Leu Val Glu Lys Met Arg Phe	
65 70 75	
aac tcc ggt ata ttg ggg aat tta aga gtg cat gca cgt ttg agg caa	467
Asn Ser Gly Ile Leu Gly Asn Leu Arg Val His Ala Arg Leu Arg Gln	
80 85 90 95	
gcc cta aaa ttg caa aag aat ttg aaa tat tgc ctt aaa atc atc gct	515
Ala Leu Lys Leu Gln Lys Asn Leu Lys Tyr Cys Leu Lys Ile Ile Ala	
100 105 110	
agg gat tct ttt tat agc tac cgc acc ggt att tat atc ccc tta ggc	563
Arg Asp Ser Phe Tyr Ser Tyr Arg Thr Gly Ile Tyr Ile Pro Leu Gly	
115 120 125	
att tct tta aaa gat caa aaa acg gct caa aaa atg ctc gct gat ttg	611
Ile Ser Leu Lys Asp Gln Lys Thr Ala Gln Lys Met Leu Ala Asp Leu	
130 135 140	
agc gtg gta ggg gcg tat ctt aaa aaa caa caa gag aat gaa aag gct	659
Ser Val Val Gly Ala Tyr Leu Lys Lys Gln Gln Glu Asn Glu Lys Ala	
145 150 155	
caa agc cct tat tac aga aac aac aac tat tac aac tct tac tat agc	707
Gln Ser Pro Tyr Tyr Arg Asn Asn Asn Tyr Tyr Asn Ser Tyr Tyr Ser	
160 165 170 175	
cct tat tac gga atg tat ggt atg tat ggc atg ggc atg tat gga atg	755
Pro Tyr Tyr Gly Met Tyr Gly Met Tyr Gly Met Gly Met Tyr Gly Met	
180 185 190	
tat ggc atg ggc atg tat gat ttt tat gac ttt tat gat ggc atg tat	803
Tyr Gly Met Gly Met Tyr Asp Phe Tyr Asp Phe Tyr Asp Gly Met Tyr	
195 200 205	
gga ttc tac cct aac atg ttt ttc atg atg caa gtt caa gat tac ttg	851
Gly Phe Tyr Pro Asn Met Phe Phe Met Met Gln Val Gln Asp Tyr Leu	
210 215 220	
atg tta gaa aat tac atg tat gcg ctc gat caa gaa gag att tta gat	899
Met Leu Glu Asn Tyr Met Tyr Ala Leu Asp Gln Glu Glu Ile Leu Asp	

225	230	235	
cat gac gct tct act gac caa ctt gat acg cct act gat gat gac aaa His Asp Ala Ser Thr Asp Gln Leu Asp Thr Pro Thr Asp Asp Asp Lys 240 245 250 255			947
gac gat aaa gac gat aaa tcc tta cag cag gca aat ctt atg aac ttt Asp Asp Lys Asp Asp Lys Ser Leu Gln Gln Ala Asn Leu Met Asn Phe 260 265 270			995
tat cgt gat ccc aaa ttc agc aaa ggc att caa acc aac cgc ttg aat Tyr Arg Asp Pro Lys Phe Ser Lys Gly Ile Gln Thr Asn Arg Leu Asn 275 280 285			1043
agc gct tta gtc aat tta gac aac agt cgc atg ctc aaa gac aat tcg Ser Ala Leu Val Asn Leu Asp Asn Ser Arg Met Leu Lys Asp Asn Ser 290 295 300			1091
ctt ttc cac act aaa gcc atg ccc act aaa agc gtg gat gcg ata act Leu Phe His Thr Lys Ala Met Pro Thr Lys Ser Val Asp Ala Ile Thr 305 310 315			1139
tct caa gcc aaa gag ctt aac cat tta gtg ggg caa atc aaa gaa atg Ser Gln Ala Lys Glu Leu Asn His Leu Val Gly Gln Ile Lys Glu Met 320 325 330 335			1187
aag caa gac ggg gcg agt cct agt aag att gat tca gtt gtc aat aaa Lys Gln Asp Gly Ala Ser Pro Ser Lys Ile Asp Ser Val Val Asn Lys 340 345 350			1235
gct atg gaa gtg agg gac aag cta gac aat aat ctc aac caa cta gac Ala Met Glu Val Arg Asp Lys Leu Asp Asn Asn Leu Asn Gln Leu Asp 355 360 365			1283
aat gac tta aaa gat caa aaa ggg ctt tca agc gag caa caa gct caa Asn Asp Leu Lys Asp Gln Lys Gly Leu Ser Ser Glu Gln Gln Ala Gln 370 375 380			1331
gtg gat aaa gcc cta gac agc gtg caa caa tta agc cat agc agc gat Val Asp Lys Ala Leu Asp Ser Val Gln Gln Leu Ser His Ser Ser Asp 385 390 395			1379
gtg gtg ggg aat tat tta gac ggg agt ttg aaa att gat ggc gat gat Val Val Gly Asn Tyr Leu Asp Gly Ser Leu Lys Ile Asp Gly Asp Asp 400 405 410 415			1427
aga gat gat ttg aat gat gcg atg aat aac cct atg caa caa ccc gtg Arg Asp Asp Leu Asn Asp Ala Met Asn Asn Pro Met Gln Gln Pro Val 420 425 430			1475
caa caa acg cct act agc aac atg gcc gac acc cat gca aat gac agc Gln Gln Thr Pro Thr Ser Asn Met Ala Asp Thr His Ala Asn Asp Ser 435 440 445			1523
aag gat caa ggg agt aac gcg ctc ata aac cct aac agc gcc act aac Lys Asp Gln Gly Ser Asn Ala Leu Ile Asn Pro Asn Ser Ala Thr Asn 450 455 460			1571

gcc gac gac act cac act gac gat act cac act gac act aac acc aca 1619
 Ala Asp Asp Thr His Thr Asp Asp Thr His Thr Asp Thr Asn Thr Thr
 465 470 475
 aac gat gct agc acc act gac acc ccc act gac gat aaa gat gct agc 1667
 Asn Asp Ala Ser Thr Thr Asp Thr Pro Thr Asp Asp Lys Asp Ala Ser
 480 485 490 495
 ggc ttg aac aat acc ggc gat atg aat aac acg gat acc ggc aac acg 1715
 Gly Leu Asn Asn Thr Gly Asp Met Asn Asn Thr Asp Thr Gly Asn Thr
 500 505 510
 gac acc ggc aat acg gat acc ggt aac act gat gat atg agc aac atg 1763
 Asp Thr Gly Asn Thr Asp Thr Gly Asn Thr Asp Asp Met Ser Asn Met
 515 520 525
 aac aac ggc aac gat gat acg ggt aac gct aat gac gac atg agc aac 1811
 Asn Asn Gly Asn Asp Asp Thr Gly Asn Ala Asn Asp Asp Met Ser Asn
 530 535 540
 ggc aac gac atg ggc gat gat ttg aac aac gcg aac gat atg aac gac 1859
 Gly Asn Asp Met Gly Asp Asp Leu Asn Asn Ala Asn Asp Met Asn Asp
 545 550 555
 gac atg ggt aat ggc aac gat gac atg ggc gat atg ggc gat atg aac 1907
 Asp Met Gly Asn Gly Asn Asp Asp Met Gly Asp Met Gly Asp Met Asn
 560 565 570 575
 gac gat atg ggt ggc gat atg gga gac atg ggc gat atg ggc gat atg 1955
 Asp Asp Met Gly Gly Asp Met Gly Asp Met Gly Asp Met Gly Asp Met
 580 585 590
 ggg aat tgagattaac cccaatatca aagagtgata gccaaaactt taaggaatat 2011
 Gly Asn

ttttatagta aaaacgattc ttttaaggta atagggggga tatttttgc 2059

<210> 66

<211> 593

<212> PRT

<213> Helicobacter pylori

<400> 66

Met Lys Ala Ile Lys Ile Leu Phe Ile Met Thr Leu Ser Leu Asn Ala
 1 5 10 15
 Ile Ser Val Asn Arg Ala Leu Phe Asp Leu Lys Asp Ser Gln Leu Lys
 20 25 30
 Gly Glu Leu Thr Pro Lys Ile Val Asn Phe Gly Gly Tyr Lys Ser Ser
 35 40 45
 Thr Glu Glu Trp Gly Ala Thr Ala Leu Asn Tyr Ile Asn Ala Ala Asn
 50 55 60
 Gly Asp Ala Lys Lys Phe Ser Thr Leu Val Glu Lys Met Arg Phe Asn
 65 70 75 80
 Ser Gly Ile Leu Gly Asn Leu Arg Val His Ala Arg Leu Arg Gln Ala
 85 90 95
 Leu Lys Leu Gln Lys Asn Leu Lys Tyr Cys Leu Lys Ile Ile Ala Arg
 100 105 110

- 83 -

Asp Met Gly Gly Asp Met Gly Asp Met Gly Asp Met Gly Asp Met Gly
 580 585 590
 Asn

<210> 67
 <211> 1527
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (112)...(1461)

<400> 67
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 ttcttatatt atgattacga tttatcaatt taaaacattt ggagaaagac a atg agt 117
 Met Ser
 1
 atg gaa ttt gat gct gtt att att gga ggt ggg gtt tca ggg tgc gcg 165
 Met Glu Phe Asp Ala Val Ile Ile Gly Gly Gly Val Ser Gly Cys Ala
 5 10 15
 acc ttt tat act ttg agc gaa tac agc tct tta aag cgc gtg gct atc 213
 Thr Phe Tyr Thr Leu Ser Glu Tyr Ser Ser Leu Lys Arg Val Ala Ile
 20 25 30
 gtg gaa aaa tgc tct aaa ttg gct caa atc agc tcc agc gct aaa gct 261
 Val Glu Lys Cys Ser Lys Leu Ala Gln Ile Ser Ser Ser Ala Lys Ala
 35 40 45 50
 aat tgc caa acc att cat gat ggc tct att gaa acg aat tac act ccc 309
 Asn Ser Gln Thr Ile His Asp Gly Ser Ile Glu Thr Asn Tyr Thr Pro
 55 60 65
 gaa aaa gct aaa aaa gtg cgt ttg agc gct tat aag acc agg caa tac 357
 Glu Lys Ala Lys Lys Val Arg Leu Ser Ala Tyr Lys Thr Arg Gln Tyr
 70 75 80
 gct ttg aat aaa ggc ttg caa aat gaa gtg att ttt gaa acc cag aaa 405
 Ala Leu Asn Lys Gly Leu Gln Asn Glu Val Ile Phe Glu Thr Gln Lys
 85 90 95
 atg gct ata ggc gtg ggc gat gaa gaa tgc gag ttc atg aaa aaa cgc 453
 Met Ala Ile Gly Val Gly Asp Glu Glu Cys Glu Phe Met Lys Lys Arg
 100 105 110
 tac gaa tct ttt aaa gaa atc ttt gtg ggg tta gaa gaa ttt gac aag 501
 Tyr Glu Ser Phe Lys Glu Ile Phe Val Gly Leu Glu Glu Phe Asp Lys
 115 120 125 130
 caa aag att aaa gaa tta gag cct aat gtg att tta ggg gct aat ggc 549
 Gln Lys Ile Lys Glu Leu Glu Pro Asn Val Ile Leu Gly Ala Asn Gly
 135 140 145
 ata gac agg cat gaa aac att atc ggg cat ggg tat aga aag gat tgg 597

Ile	Asp	Arg	His	Glu	Asn	Ile	Ile	Gly	His	Gly	Tyr	Arg	Lys	Asp	Trp	
			150					155					160			
agc	acc	atg	aat	ttt	gcg	aag	ttg	agt	gaa	aac	ttc	gtt	gaa	gaa	gcc	645
Ser	Thr	Met	Asn	Phe	Ala	Lys	Leu	Ser	Glu	Asn	Phe	Val	Glu	Glu	Ala	
		165					170					175				
cta	aaa	tta	aag	cct	aac	aac	cag	gtg	ttt	ttg	aat	ttc	aaa	gtg	aaa	693
Leu	Lys	Leu	Lys	Pro	Asn	Asn	Gln	Val	Phe	Leu	Asn	Phe	Lys	Val	Lys	
	180						185					190				
aag	att	gaa	aaa	cgc	aac	gac	act	tac	gcc	gta	att	tca	gaa	gac	gct	741
Lys	Ile	Glu	Lys	Arg	Asn	Asp	Thr	Tyr	Ala	Val	Ile	Ser	Glu	Asp	Ala	
195					200					205					210	
gaa	gaa	gtg	tat	gct	aaa	ttc	gtg	ctg	gtc	aat	gcc	ggc	tct	tac	gct	789
Glu	Glu	Val	Tyr	Ala	Lys	Phe	Val	Leu	Val	Asn	Ala	Gly	Ser	Tyr	Ala	
				215					220					225		
ttg	cct	ttg	gct	cag	agc	atg	ggc	tat	ggc	cta	gat	tta	ggg	tgc	ttg	837
Leu	Pro	Leu	Ala	Gln	Ser	Met	Gly	Tyr	Gly	Leu	Asp	Leu	Gly	Cys	Leu	
			230					235					240			
cct	gtg	gcg	ggc	agc	ttt	tat	ttt	gtg	ccg	gat	tta	tta	agg	ggg	aag	885
Pro	Val	Ala	Gly	Ser	Phe	Tyr	Phe	Val	Pro	Asp	Leu	Leu	Arg	Gly	Lys	
		245					250					255				
gtt	tat	acc	gtt	caa	aac	ccc	aaa	ctc	cct	ttt	gca	gcc	gtg	cat	ggc	933
Val	Tyr	Thr	Val	Gln	Asn	Pro	Lys	Leu	Pro	Phe	Ala	Ala	Val	His	Gly	
	260					265					270					
gac	cct	gat	gcc	gtc	att	aaa	gga	aaa	aca	cga	atc	ggg	cct	acc	gct	981
Asp	Pro	Asp	Ala	Val	Ile	Lys	Gly	Lys	Thr	Arg	Ile	Gly	Pro	Thr	Ala	
275					280					285					290	
tta	acg	atg	cct	aaa	tta	gaa	cgc	aac	aaa	tgt	tgg	ctt	aag	ggc	att	1029
Leu	Thr	Met	Pro	Lys	Leu	Glu	Arg	Asn	Lys	Cys	Trp	Leu	Lys	Gly	Ile	
				295					300					305		
agc	ttg	gaa	ttg	ttg	aaa	atg	gat	ttg	aat	aaa	gat	gtg	ttt	aaa	att	1077
Ser	Leu	Glu	Leu	Leu	Lys	Met	Asp	Leu	Asn	Lys	Asp	Val	Phe	Lys	Ile	
			310					315					320			
gcg	ttt	gat	ttg	atg	agc	gat	aaa	gaa	atc	cga	aat	tat	gtg	ttt	aaa	1125
Ala	Phe	Asp	Leu	Met	Ser	Asp	Lys	Glu	Ile	Arg	Asn	Tyr	Val	Phe	Lys	
		325					330					335				
aac	atg	gtt	ttt	gaa	ttg	ccc	att	atc	ggg	aaa	agg	aaa	ttt	tta	aaa	1173
Asn	Met	Val	Phe	Glu	Leu	Pro	Ile	Ile	Gly	Lys	Arg	Lys	Phe	Leu	Lys	
	340					345					350					
gac	gct	caa	aaa	atc	atc	ccc	tct	ctt	agc	cta	gaa	gat	cta	gaa	tac	1221
Asp	Ala	Gln	Lys	Ile	Ile	Pro	Ser	Leu	Ser	Leu	Glu	Asp	Leu	Glu	Tyr	
355					360					365					370	
gct	cat	ggg	ttt	ggg	gaa	gtg	cgc	ccg	caa	gtt	tta	gac	aga	acc	aag	1269
Ala	His	Gly	Phe	Gly	Glu	Val	Arg	Pro	Gln	Val	Leu	Asp	Arg	Thr	Lys	
				375					380					385		

cga aaa ctg gaa tta ggc gaa aaa aag att tgc acc cat aaa ggc atc 1317
 Arg Lys Leu Glu Leu Gly Glu Lys Lys Ile Cys Thr His Lys Gly Ile
 390 395 400

act ttt aac atg acc cct tct cca ggc gcg acg agt tgt ttg caa aac 1365
 Thr Phe Asn Met Thr Pro Ser Pro Gly Ala Thr Ser Cys Leu Gln Asn
 405 410 415

gcc ctt gtg gat tcc caa gaa atc gct gcg tat ttg ggc gag agc ttt 1413
 Ala Leu Val Asp Ser Gln Glu Ile Ala Ala Tyr Leu Gly Glu Ser Phe
 420 425 430

gaa tta gaa cgc ttt tat aaa gat tta tcc cca gaa gaa ttg gaa aat 1461
 Glu Leu Glu Arg Phe Tyr Lys Asp Leu Ser Pro Glu Glu Leu Glu Asn
 435 440 445 450

taaaaacgca tgcaaaaaga acaagaagcc caagaaatcg ctaaaaaagc cgttaaaatc 1521
 gtgttt 1527

<210> 68
 <211> 450
 <212> PRT
 <213> Helicobacter pylori

<400> 68
 Met Ser Met Glu Phe Asp Ala Val Ile Ile Gly Gly Gly Val Ser Gly
 1 5 10 15
 Cys Ala Thr Phe Tyr Thr Leu Ser Glu Tyr Ser Ser Leu Lys Arg Val
 20 25 30
 Ala Ile Val Glu Lys Cys Ser Lys Leu Ala Gln Ile Ser Ser Ser Ala
 35 40 45
 Lys Ala Asn Ser Gln Thr Ile His Asp Gly Ser Ile Glu Thr Asn Tyr
 50 55 60
 Thr Pro Glu Lys Ala Lys Lys Val Arg Leu Ser Ala Tyr Lys Thr Arg
 65 70 75 80
 Gln Tyr Ala Leu Asn Lys Gly Leu Gln Asn Glu Val Ile Phe Glu Thr
 85 90 95
 Gln Lys Met Ala Ile Gly Val Gly Asp Glu Glu Cys Glu Phe Met Lys
 100 105 110
 Lys Arg Tyr Glu Ser Phe Lys Glu Ile Phe Val Gly Leu Glu Glu Phe
 115 120 125
 Asp Lys Gln Lys Ile Lys Glu Leu Glu Pro Asn Val Ile Leu Gly Ala
 130 135 140
 Asn Gly Ile Asp Arg His Glu Asn Ile Ile Gly His Gly Tyr Arg Lys
 145 150 155 160
 Asp Trp Ser Thr Met Asn Phe Ala Lys Leu Ser Glu Asn Phe Val Glu
 165 170 175
 Glu Ala Leu Lys Leu Lys Pro Asn Asn Gln Val Phe Leu Asn Phe Lys
 180 185 190
 Val Lys Lys Ile Glu Lys Arg Asn Asp Thr Tyr Ala Val Ile Ser Glu
 195 200 205
 Asp Ala Glu Glu Val Tyr Ala Lys Phe Val Leu Val Asn Ala Gly Ser
 210 215 220
 Tyr Ala Leu Pro Leu Ala Gln Ser Met Gly Tyr Gly Leu Asp Leu Gly
 225 230 235 240
 Cys Leu Pro Val Ala Gly Ser Phe Tyr Phe Val Pro Asp Leu Leu Arg
 245 250 255

Gly Lys Val Tyr Thr Val Gln Asn Pro Lys Leu Pro Phe Ala Ala Val
 260 265 270
 His Gly Asp Pro Asp Ala Val Ile Lys Gly Lys Thr Arg Ile Gly Pro
 275 280 285
 Thr Ala Leu Thr Met Pro Lys Leu Glu Arg Asn Lys Cys Trp Leu Lys
 290 295 300
 Gly Ile Ser Leu Glu Leu Leu Lys Met Asp Leu Asn Lys Asp Val Phe
 305 310 315 320
 Lys Ile Ala Phe Asp Leu Met Ser Asp Lys Glu Ile Arg Asn Tyr Val
 325 330 335
 Phe Lys Asn Met Val Phe Glu Leu Pro Ile Ile Gly Lys Arg Lys Phe
 340 345 350
 Leu Lys Asp Ala Gln Lys Ile Ile Pro Ser Leu Ser Leu Glu Asp Leu
 355 360 365
 Glu Tyr Ala His Gly Phe Gly Glu Val Arg Pro Gln Val Leu Asp Arg
 370 375 380
 Thr Lys Arg Lys Leu Glu Leu Gly Glu Lys Lys Ile Cys Thr His Lys
 385 390 395 400
 Gly Ile Thr Phe Asn Met Thr Pro Ser Pro Gly Ala Thr Ser Cys Leu
 405 410 415
 Gln Asn Ala Leu Val Asp Ser Gln Glu Ile Ala Ala Tyr Leu Gly Glu
 420 425 430
 Ser Phe Glu Leu Glu Arg Phe Tyr Lys Asp Leu Ser Pro Glu Glu Leu
 435 440 445
 Glu Asn
 450

<210> 69
 <211> 653
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (63)...(590)

<400> 69
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 gc atg cca aaa ccc aag aaa aac acc ctc ccc tgt agc ctt tct gtc 107
 Met Pro Lys Pro Lys Lys Asn Thr Leu Pro Cys Ser Leu Ser Val
 1 5 10 15
 aaa atg tct tat ttc atg cgc ttt ctc att aaa tgg cgc acc cgc tct 155
 Lys Met Ser Tyr Phe Met Arg Phe Leu Ile Lys Trp Arg Thr Arg Ser
 20 25 30
 tta agc cat aaa atg atg act ctc att caa atc tta agc att ctg gct 203
 Leu Ser His Lys Met Met Thr Leu Ile Gln Ile Leu Ser Ile Leu Ala
 35 40 45
 tta gcg agc aag gcc agt gaa gat tta gaa gag caa ctc aaa aaa atc 251
 Leu Ala Ser Lys Ala Ser Glu Asp Leu Glu Glu Gln Leu Lys Lys Ile
 50 55 60
 aaa gat tac att tat aga acc cta aac gct aaa atc gca tcg gat gtg 299
 Lys Asp Tyr Ile Tyr Arg Thr Leu Asn Ala Lys Ile Ala Ser Asp Val
 65 70 75

tat aac cga gtg ctt att tta gtg aat gaa tat tgc act aat gaa gaa	347
Tyr Asn Arg Val Leu Ile Leu Val Asn Glu Tyr Cys Thr Asn Glu Glu	
80 85 90 95	
ttg ttt gac aaa gag agc gtt aaa att tca gat tta ctc att caa gac	395
Leu Phe Asp Lys Glu Ser Val Lys Ile Ser Asp Leu Leu Ile Gln Asp	
100 105 110	
att cag ctt tac gct tta gtg gat gaa atg ctt aaa gaa gat aaa tat	443
Ile Gln Leu Tyr Ala Leu Val Asp Glu Met Leu Lys Glu Asp Lys Tyr	
115 120 125	
caa gtc cag cac acc att tta aag ggc atc atc aaa cgc aaa tac gat	491
Gln Val Gln His Thr Ile Leu Lys Gly Ile Ile Lys Arg Lys Tyr Asp	
130 135 140	
gaa gcc tac tcg ctc aat agc gaa gac agg att ctt tta gaa tac caa	539
Glu Ala Tyr Ser Leu Asn Ser Glu Asp Arg Ile Leu Leu Glu Tyr Gln	
145 150 155	
gaa cgc ttg cta gaa cac tca cac gcg tct ttt tca aat aaa aaa ttc	587
Glu Arg Leu Leu Glu His Ser His Ala Ser Phe Ser Asn Lys Lys Phe	
160 165 170 175	
aaa tgatttgaaa gcgttacttg ccttgctttt tgggctttta ttgaaaaagg	640
Lys	

gcttttaaaat gag	653
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<210> 70
 <211> 176
 <212> PRT
 <213> Helicobacter pylori

<400> 70	
Met Pro Lys Pro Lys Lys Asn Thr Leu Pro Cys Ser Leu Ser Val Lys	
1 5 10 15	
Met Ser Tyr Phe Met Arg Phe Leu Ile Lys Trp Arg Thr Arg Ser Leu	
20 25 30	
Ser His Lys Met Met Thr Leu Ile Gln Ile Leu Ser Ile Leu Ala Leu	
35 40 45	
Ala Ser Lys Ala Ser Glu Asp Leu Glu Glu Gln Leu Lys Lys Ile Lys	
50 55 60	
Asp Tyr Ile Tyr Arg Thr Leu Asn Ala Lys Ile Ala Ser Asp Val Tyr	
65 70 75 80	
Asn Arg Val Leu Ile Leu Val Asn Glu Tyr Cys Thr Asn Glu Glu Leu	
85 90 95	
Phe Asp Lys Glu Ser Val Lys Ile Ser Asp Leu Leu Ile Gln Asp Ile	
100 105 110	
Gln Leu Tyr Ala Leu Val Asp Glu Met Leu Lys Glu Asp Lys Tyr Gln	
115 120 125	
Val Gln His Thr Ile Leu Lys Gly Ile Ile Lys Arg Lys Tyr Asp Glu	
130 135 140	
Ala Tyr Ser Leu Asn Ser Glu Asp Arg Ile Leu Leu Glu Tyr Gln Glu	
145 150 155 160	
Arg Leu Leu Glu His Ser His Ala Ser Phe Ser Asn Lys Lys Phe Lys	

165

170

175

<210> 71

<211> 1840

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (91)...(1833)

<400> 71

aagcgtaaaa ttccaatcaa aaaccatcgt atcgggtgta atattgtgta aaaattaatg 60

ttatgaatct cttgtatttaa aaggacttca atg aaa aaa ttg gtt tta gtc atc 114

Met Lys Lys Leu Val Leu Val Ile

1

5

ttt tta acg cta gcg ctt tca ata tct gca aaa gaa gtc aaa ata gtg 162

Phe Leu Thr Leu Ala Leu Ser Ile Ser Ala Lys Glu Val Lys Ile Val

10

15

20

ttt tta gaa act tca gac att cat ggg cgg ctt ttt tcg tat gat tat 210

Phe Leu Glu Thr Ser Asp Ile His Gly Arg Leu Phe Ser Tyr Asp Tyr

25

30

35

40

gcg att ggc gag caa aaa ccc aat aac ggc ttg aca agg att gcg act 258

Ala Ile Gly Glu Gln Lys Pro Asn Asn Gly Leu Thr Arg Ile Ala Thr

45

50

55

tta atc aaa aag caa agg gct gag aat aaa aat gtg gtt ttg att gac 306

Leu Ile Lys Lys Gln Arg Ala Glu Asn Lys Asn Val Val Leu Ile Asp

60

65

70

agc ggg gat ttg ttg caa ggc aat agc gcg gag ttg ttt aat gat gag 354

Ser Gly Asp Leu Leu Gln Gly Asn Ser Ala Glu Leu Phe Asn Asp Glu

75

80

85

cca att cat ccg cta gtt aga gct gaa aac gat ttg aaa ttt gac att 402

Pro Ile His Pro Leu Val Arg Ala Glu Asn Asp Leu Lys Phe Asp Ile

90

95

100

cgt gtg ctt ggc aat cac gag ttt aat ttc agt aaa gat ttt tta gaa 450

Arg Val Leu Gly Asn His Glu Phe Asn Phe Ser Lys Asp Phe Leu Glu

105

110

115

120

aag aat att aag ggg ttt aat ggc gat gtc atg aat gcg aat atc att 498

Lys Asn Ile Lys Gly Phe Asn Gly Asp Val Met Asn Ala Asn Ile Ile

125

130

135

aaa att gcg gac aat aag ccg ttt gta aaa cct tat att att aaa aaa 546

Lys Ile Ala Asp Asn Lys Pro Phe Val Lys Pro Tyr Ile Ile Lys Lys

140

145

150

att gat ggc gtg agg gtg gcg gtt gtg ggg tat gtg gtg gcg cac atc 594

Ile Asp Gly Val Arg Val Ala Val Val Gly Tyr Val Val Ala His Ile

155

160

165

cca act tgg gag gcc tct acg cct gaa cat ttt gca gga ttg aag ttt	642
Pro Thr Trp Glu Ala Ser Thr Pro Glu His Phe Ala Gly Leu Lys Phe	
170 175 180	
ttg gac gct gaa gaa gcg tta aaa aag acc tta aaa gag ttg aaa ggg	690
Leu Asp Ala Glu Glu Ala Leu Lys Lys Thr Leu Lys Glu Leu Lys Gly	
185 190 195 200	
aag tat gat att ttg att ggc gct ttt cat ttg ggg cga gaa gat gag	738
Lys Tyr Asp Ile Leu Ile Gly Ala Phe His Leu Gly Arg Glu Asp Glu	
205 210 215	
aaa ggt ggc gac ggg ata ccg gat tta gcg aaa aaa ttc ccg caa ttt	786
Lys Gly Gly Asp Gly Ile Pro Asp Leu Ala Lys Lys Phe Pro Gln Phe	
220 225 230	
gac atc att ttt gca ggg cat gag cat gcg gtt tat aac acc aaa gta	834
Asp Ile Ile Phe Ala Gly His Glu His Ala Val Tyr Asn Thr Lys Val	
235 240 245	
ggg aaa gtg cat acc att gag cct gga gcg tat ggg gct tat ctg gca	882
Gly Lys Val His Thr Ile Glu Pro Gly Ala Tyr Gly Ala Tyr Leu Ala	
250 255 260	
aag ggc gtg gtg gta ttt gac act aaa acg aag aaa aaa att ata acg	930
Lys Gly Val Val Val Phe Asp Thr Lys Thr Lys Lys Lys Ile Ile Thr	
265 270 275 280	
act gaa aat tta ccc aca aaa gat gtg cca gaa gat gaa gaa tta gcg	978
Thr Glu Asn Leu Pro Thr Lys Asp Val Pro Glu Asp Glu Glu Leu Ala	
285 290 295	
aaa aaa tac gaa tat gtg gat aaa aaa tca aaa gaa tac gct aat gaa	1026
Lys Lys Tyr Glu Tyr Val Asp Lys Lys Ser Lys Glu Tyr Ala Asn Glu	
300 305 310	
gtg gtt ggc gaa gtt aca aaa acc ttt att gac agg cct gat ttt atc	1074
Val Val Gly Glu Val Thr Lys Thr Phe Ile Asp Arg Pro Asp Phe Ile	
315 320 325	
aca gga gaa gaa aaa atc acc acg atg ccc acc gcc gcc ttg caa gaa	1122
Thr Gly Glu Glu Lys Ile Thr Thr Met Pro Thr Ala Ala Leu Gln Glu	
330 335 340	
aca ccg gtg ata gaa ttg att aat aaa gtg caa aaa tat tac gca aaa	1170
Thr Pro Val Ile Glu Leu Ile Asn Lys Val Gln Lys Tyr Tyr Ala Lys	
345 350 355 360	
gcc gat gtt tca gcg gca gcc tta ttc aat ttt ggg gcg aat ttg aaa	1218
Ala Asp Val Ser Ala Ala Leu Phe Asn Phe Gly Ala Asn Leu Lys	
365 370 375	
aaa ggg cct ttc aaa aga aaa gat gtc act tat att tac aag ttc gct	1266
Lys Gly Pro Phe Lys Arg Lys Asp Val Thr Tyr Ile Tyr Lys Phe Ala	
380 385 390	
aat acg ctc att gga gtg cgt ata acg ggt gaa aat ctg ttg aaa tac	1314
Asn Thr Leu Ile Gly Val Arg Ile Thr Gly Glu Asn Leu Leu Lys Tyr	

395	400	405	
atg gaa tgg tca tac cga ttt tac aat cag ttg caa cca gga gat ttg Met Glu Trp Ser Tyr Arg Phe Tyr Asn Gln Leu Gln Pro Gly Asp Leu 410 415 420			1362
acg atc agt ttt aat gaa aac att cgc ggc tat aac ttt gat atg ttt Thr Ile Ser Phe Asn Glu Asn Ile Arg Gly Tyr Asn Phe Asp Met Phe 425 430 435 440			1410
tct ggc gtg aaa tac cag gtt gat gtt aca aaa ccc gcc gga caa agg Ser Gly Val Lys Tyr Gln Val Asp Val Thr Lys Pro Ala Gly Gln Arg 445 450 455			1458
att atc aat ccg aca atc aac aac aaa ccc att gac ccc aaa gcc atc Ile Ile Asn Pro Thr Ile Asn Asn Lys Pro Ile Asp Pro Lys Ala Ile 460 465 470			1506
tat aaa tta gcg atc aac aat tac cga ttc gga aca tta tcc acg aca Tyr Lys Leu Ala Ile Asn Asn Tyr Arg Phe Gly Thr Leu Ser Thr Thr 475 480 485			1554
ttg aat ttg gtt aca gac gct gmt agg tat tat aat tct tac gat gaa Leu Asn Leu Val Thr Asp Ala Xaa Arg Tyr Tyr Asn Ser Tyr Asp Glu 490 495 500			1602
ctg caa gat aat ggg caa ata cga gat ttg atc atc aaa tac atc acg Leu Gln Asp Asn Gly Gln Ile Arg Asp Leu Ile Ile Lys Tyr Ile Thr 505 510 515 520			1650
gaa gaa aaa ggt ggg aag gta acc cct gaa ttg gag ggt aat tgg gaa Glu Glu Lys Gly Gly Lys Val Thr Pro Glu Leu Glu Gly Asn Trp Glu 525 530 535			1698
atc atc aac tac gat ttc aaa aac ccg ttg ttg gaa aaa ttg aga gaa Ile Ile Asn Tyr Asp Phe Lys Asn Pro Leu Leu Glu Lys Leu Arg Glu 540 545 550			1746
aaa tta aaa gag ggg agc atc aaa atc ccc acc tca aag gat ggg agg Lys Leu Lys Glu Gly Ser Ile Lys Ile Pro Thr Ser Lys Asp Gly Arg 555 560 565			1794
act ttg aat gtc aaa tcc att aaa gag agt gaa gtt aaa taaaatt Thr Leu Asn Val Lys Ser Ile Lys Glu Ser Glu Val Lys 570 575 580			1840

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<211> 581

<212> PRT

<213> Helicobacter pylori

<400> 72

Met Lys Lys Leu Val Leu Val Ile Phe Leu Thr Leu Ala Leu Ser Ile 1 5 10 15
Ser Ala Lys Glu Val Lys Ile Val Phe Leu Glu Thr Ser Asp Ile His 20 25 30
Gly Arg Leu Phe Ser Tyr Asp Tyr Ala Ile Gly Glu Gln Lys Pro Asn

	35					40				45					
Asn	Gly	Leu	Thr	Arg	Ile	Ala	Thr	Leu	Ile	Lys	Lys	Gln	Arg	Ala	Glu
50						55					60				
Asn	Lys	Asn	Val	Val	Leu	Ile	Asp	Ser	Gly	Asp	Leu	Leu	Gln	Gly	Asn
65					70					75					80
Ser	Ala	Glu	Leu	Phe	Asn	Asp	Glu	Pro	Ile	His	Pro	Leu	Val	Arg	Ala
				85					90					95	
Glu	Asn	Asp	Leu	Lys	Phe	Asp	Ile	Arg	Val	Leu	Gly	Asn	His	Glu	Phe
			100					105					110		
Asn	Phe	Ser	Lys	Asp	Phe	Leu	Glu	Lys	Asn	Ile	Lys	Gly	Phe	Asn	Gly
			115					120					125		
Asp	Val	Met	Asn	Ala	Asn	Ile	Ile	Lys	Ile	Ala	Asp	Asn	Lys	Pro	Phe
			130				135						140		
Val	Lys	Pro	Tyr	Ile	Ile	Lys	Lys	Ile	Asp	Gly	Val	Arg	Val	Ala	Val
145					150					155					160
Val	Gly	Tyr	Val	Val	Ala	His	Ile	Pro	Thr	Trp	Glu	Ala	Ser	Thr	Pro
				165					170					175	
Glu	His	Phe	Ala	Gly	Leu	Lys	Phe	Leu	Asp	Ala	Glu	Glu	Ala	Leu	Lys
			180					185					190		
Lys	Thr	Leu	Lys	Glu	Leu	Lys	Gly	Lys	Tyr	Asp	Ile	Leu	Ile	Gly	Ala
			195					200					205		
Phe	His	Leu	Gly	Arg	Glu	Asp	Glu	Lys	Gly	Gly	Asp	Gly	Ile	Pro	Asp
			210				215						220		
Leu	Ala	Lys	Lys	Phe	Pro	Gln	Phe	Asp	Ile	Ile	Phe	Ala	Gly	His	Glu
225					230					235					240
His	Ala	Val	Tyr	Asn	Thr	Lys	Val	Gly	Lys	Val	His	Thr	Ile	Glu	Pro
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Gly	Ala	Tyr	Gly	Ala	Tyr	Leu	Ala	Lys	Gly	Val	Val	Val	Phe	Asp	Thr
			260					265					270		
Lys	Thr	Lys	Lys	Lys	Ile	Ile	Thr	Thr	Glu	Asn	Leu	Pro	Thr	Lys	Asp
			275					280					285		
Val	Pro	Glu	Asp	Glu	Glu	Leu	Ala	Lys	Lys	Tyr	Glu	Tyr	Val	Asp	Lys
			290				295				300				
Lys	Ser	Lys	Glu	Tyr	Ala	Asn	Glu	Val	Val	Gly	Glu	Val	Thr	Lys	Thr
305					310					315					320
Phe	Ile	Asp	Arg	Pro	Asp	Phe	Ile	Thr	Gly	Glu	Glu	Lys	Ile	Thr	Thr
				325					330					335	
Met	Pro	Thr	Ala	Ala	Leu	Gln	Glu	Thr	Pro	Val	Ile	Glu	Leu	Ile	Asn
			340					345					350		
Lys	Val	Gln	Lys	Tyr	Tyr	Ala	Lys	Ala	Asp	Val	Ser	Ala	Ala	Ala	Leu
			355					360					365		
Phe	Asn	Phe	Gly	Ala	Asn	Leu	Lys	Lys	Gly	Pro	Phe	Lys	Arg	Lys	Asp
			370				375				380				
Val	Thr	Tyr	Ile	Tyr	Lys	Phe	Ala	Asn	Thr	Leu	Ile	Gly	Val	Arg	Ile
385					390					395					400
Thr	Gly	Glu	Asn	Leu	Leu	Lys	Tyr	Met	Glu	Trp	Ser	Tyr	Arg	Phe	Tyr
				405					410					415	
Asn	Gln	Leu	Gln	Pro	Gly	Asp	Leu	Thr	Ile	Ser	Phe	Asn	Glu	Asn	Ile
			420					425					430		
Arg	Gly	Tyr	Asn	Phe	Asp	Met	Phe	Ser	Gly	Val	Lys	Tyr	Gln	Val	Asp
			435				440						445		
Val	Thr	Lys	Pro	Ala	Gly	Gln	Arg	Ile	Ile	Asn	Pro	Thr	Ile	Asn	Asn
			450				455						460		
Lys	Pro	Ile	Asp	Pro	Lys	Ala	Ile	Tyr	Lys	Leu	Ala	Ile	Asn	Asn	Tyr
465					470					475					480
Arg	Phe	Gly	Thr	Leu	Ser	Thr	Thr	Leu	Asn	Leu	Val	Thr	Asp	Ala	Xaa
				485					490					495	
Arg	Tyr	Tyr	Asn	Ser	Tyr	Asp	Glu	Leu	Gln	Asp	Asn	Gly	Gln	Ile	Arg

		500					505				510				
Asp	Leu	Ile	Ile	Lys	Tyr	Ile	Thr	Glu	Glu	Lys	Gly	Gly	Lys	Val	Thr
		515					520				525				
Pro	Glu	Leu	Glu	Gly	Asn	Trp	Glu	Ile	Ile	Asn	Tyr	Asp	Phe	Lys	Asn
		530				535				540					
Pro	Leu	Leu	Glu	Lys	Leu	Arg	Glu	Lys	Leu	Lys	Glu	Gly	Ser	Ile	Lys
545					550				555					560	
Ile	Pro	Thr	Ser	Lys	Asp	Gly	Arg	Thr	Leu	Asn	Val	Lys	Ser	Ile	Lys
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Glu	Ser	Glu	Val	Lys											
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 <212> DNA
 <213> Helicobacter pylori

<220>
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 gttggta atg gaa tca gta aaa aca gga aaa aca aat aag gtt ggc aag 109
 Met Glu Ser Val Lys Thr Gly Lys Thr Asn Lys Val Gly Lys
 1 5 10

aat aca gag atg gct aat aca aag gca aat aaa gag gct cat ttt aaa 157
 Asn Thr Glu Met Ala Asn Thr Lys Ala Asn Lys Glu Ala His Phe Lys
 15 20 25 30

caa gcg agc acc att aca aat ata atc aga tca att cgt ggg att ttt 205
 Gln Ala Ser Thr Ile Thr Asn Ile Ile Arg Ser Ile Arg Gly Ile Phe
 35 40 45

aca aaa att gca aag aaa gtt aga gga ctt gta aaa aaa cac ccc aag 253
 Thr Lys Ile Ala Lys Lys Val Arg Gly Leu Val Lys Lys His Pro Lys
 50 55 60

aaa agc agt gcg gca tta gta gta ttg acc cat att gcg tgc aag aaa 301
 Lys Ser Ser Ala Ala Leu Val Val Leu Thr His Ile Ala Cys Lys Lys
 65 70 75

gcg aaa gaa tta gac gat aaa gtc caa gat aaa tcc aaa caa gct gaa 349
 Ala Lys Glu Leu Asp Asp Lys Val Gln Asp Lys Ser Lys Gln Ala Glu
 80 85 90

aaa gaa aat caa atc aat tgg tgg aaa tat tca gga tta aca ata gcg 397
 Lys Glu Asn Gln Ile Asn Trp Trp Lys Tyr Ser Gly Leu Thr Ile Ala
 95 100 105 110

aca agt tta tta tta gcc gct tgt agc act ggt gat gtt agt gaa caa 445
 Thr Ser Leu Leu Leu Ala Ala Cys Ser Thr Gly Asp Val Ser Glu Gln
 115 120 125

ata gaa cta gaa caa gaa aaa caa aag acg agc aat ata gag act aac 493
 Ile Glu Leu Glu Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn

130										135										140										
aat	caa	ata	aaa	gta	gaa	caa	gaa	aaa	caa	aag	aca	agc	aat	ata	gag	541														
Asn	Gln	Ile	Lys	Val	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Ser	Asn	Ile	Glu															
		145					150					155																		
act	aat	aat	caa	ata	aaa	gta	gaa	caa	gaa	caa	caa	aag	aca	agc	aat	589														
Thr	Asn	Asn	Gln	Ile	Lys	Val	Glu	Gln	Glu	Gln	Gln	Lys	Thr	Ser	Asn															
	160					165					170																			
aca	cag	aaa	gat	ttg	gtt	aaa	gaa	cag	aaa	gat	ttg	gtt	aaa	gaa	cag	637														
Thr	Gln	Lys	Asp	Leu	Val	Lys	Glu	Gln	Lys	Asp	Leu	Val	Lys	Glu	Gln															
	175				180					185					190															
aaa	gat	ttg	gtt	aaa	gaa	cag	aaa	gat	ttg	gtt	aaa	gaa	cag	aaa	gat	685														
Lys	Asp	Leu	Val	Lys	Glu	Gln	Lys	Asp	Leu	Val	Lys	Glu	Gln	Lys	Asp															
			195					200						205																
ttg	gtt	aaa	aca	cag	aaa	gat	ttc	att	aaa	tat	gta	gaa	caa	aat	tgc	733														
Leu	Val	Lys	Thr	Gln	Lys	Asp	Phe	Ile	Lys	Tyr	Val	Glu	Gln	Asn	Cys															
		210					215						220																	
caa	gaa	aat	cat	aat	caa	ttc	ttt	att	gaa	aaa	gga	gga	att	aag	gct	781														
Gln	Glu	Asn	His	Asn	Gln	Phe	Phe	Ile	Glu	Lys	Gly	Gly	Ile	Lys	Ala															
		225				230						235																		
ggt	att	ggt	ata	gaa	gta	gaa	gct	gaa	tgc	aaa	acc	cct	aaa	cct	gca	829														
Gly	Ile	Gly	Ile	Glu	Val	Glu	Ala	Glu	Cys	Lys	Thr	Pro	Lys	Pro	Ala															
	240					245					250																			
aaa	acc	aat	caa	acc	cct	atc	cag	cca	aaa	cac	ctc	cca	aac	tct	aaa	877														
Lys	Thr	Asn	Gln	Thr	Pro	Ile	Gln	Pro	Lys	His	Leu	Pro	Asn	Ser	Lys															
	255				260					265					270															
caa	ccc	cgc	tct	caa	aga	gga	tca	aaa	gcg	caa	gag	ctt	atc	gct	tat	925														
Gln	Pro	Arg	Ser	Gln	Arg	Gly	Ser	Lys	Ala	Gln	Glu	Leu	Ile	Ala	Tyr															
			275						280					285																
ttg	caa	aaa	gag	cta	gaa	ttt	ctg	ccc	tat	tcg	caa	aaa	gct	atc	gct	973														
Leu	Gln	Lys	Glu	Leu	Glu	Phe	Leu	Pro	Tyr	Ser	Gln	Lys	Ala	Ile	Ala															
		290					295						300																	
aaa	caa	gtg	gat	ttt	tac	agg	cca	agt	tct	atc	gct	tat	tta	gaa	cta	1021														
Lys	Gln	Val	Asp	Phe	Tyr	Arg	Pro	Ser	Ser	Ile	Ala	Tyr	Leu	Glu	Leu															
		305					310					315																		
gat	cct	aga	gat	ttt	aag	gtt	aca	gaa	gaa	tggt	caa	aaa	gaa	aat	cta	1069														
Asp	Pro	Arg	Asp	Phe	Lys	Val	Thr	Glu	Glu	Trp	Gln	Lys	Glu	Asn	Leu															
	320					325					330																			
aaa	ata	cgc	tct	aaa	gct	caa	gct	aaa	atg	ctt	gaa	atg	aga	aac	cca	1117														
Lys	Ile	Arg	Ser	Lys	Ala	Gln	Ala	Lys	Met	Leu	Glu	Met	Arg	Asn	Pro															
	335				340					345					350															
caa	gcc	cac	ctt	tca	aac	tct	caa	agc	ctt	ttg	ttc	gtt	caa	aaa	ata	1165														
Gln	Ala	His	Leu	Ser	Asn	Ser	Gln	Ser	Leu	Leu	Phe	Val	Gln	Lys	Ile															
			355						360					365																

ttt gct gat gtt aat aaa gaa ata gaa gca gtt gct aat act gaa aag 1213
Phe Ala Asp Val Asn Lys Glu Ile Glu Ala Val Ala Asn Thr Glu Lys
370 375 380

aaa gca gaa aaa gcg ggt tat ggt tat agt aaa agg atg tagcgggtaa 1262
Lys Ala Glu Lys Ala Gly Tyr Gly Tyr Ser Lys Arg Met
385 390 395

aaacattgca ccaagttttt aattatctgt cggcttttga aaacattttt tatggtagcg 1322
ttatttgga ataaaag 1339

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<211> 395
<212> PRT
<213> Helicobacter pylori

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Glu Met Ala Asn Thr Lys Ala Asn Lys Glu Ala His Phe Lys Gln Ala
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Ser Thr Ile Thr Asn Ile Ile Arg Ser Ile Arg Gly Ile Phe Thr Lys
35 40 45
Ile Ala Lys Lys Val Arg Gly Leu Val Lys Lys His Pro Lys Lys Ser
50 55 60
Ser Ala Ala Leu Val Val Leu Thr His Ile Ala Cys Lys Lys Ala Lys
65 70 75 80
Glu Leu Asp Asp Lys Val Gln Asp Lys Ser Lys Gln Ala Glu Lys Glu
85 90 95
Asn Gln Ile Asn Trp Trp Lys Tyr Ser Gly Leu Thr Ile Ala Thr Ser
100 105 110
Leu Leu Leu Ala Ala Cys Ser Thr Gly Asp Val Ser Glu Gln Ile Glu
115 120 125
Leu Glu Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln
130 135 140
Ile Lys Val Glu Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn
145 150 155 160
Asn Gln Ile Lys Val Glu Gln Glu Gln Lys Thr Ser Asn Thr Gln
165 170 175
Lys Asp Leu Val Lys Glu Gln Lys Asp Leu Val Lys Glu Gln Lys Asp
180 185 190
Leu Val Lys Glu Gln Lys Asp Leu Val Lys Glu Gln Lys Asp Leu Val
195 200 205
Lys Thr Gln Lys Asp Phe Ile Lys Tyr Val Glu Gln Asn Cys Gln Glu
210 215 220
Asn His Asn Gln Phe Phe Ile Glu Lys Gly Gly Ile Lys Ala Gly Ile
225 230 235 240
Gly Ile Glu Val Glu Ala Glu Cys Lys Thr Pro Lys Pro Ala Lys Thr
245 250 255
Asn Gln Thr Pro Ile Gln Pro Lys His Leu Pro Asn Ser Lys Gln Pro
260 265 270
Arg Ser Gln Arg Gly Ser Lys Ala Gln Glu Leu Ile Ala Tyr Leu Gln
275 280 285
Lys Glu Leu Glu Phe Leu Pro Tyr Ser Gln Lys Ala Ile Ala Lys Gln
290 295 300
Val Asp Phe Tyr Arg Pro Ser Ser Ile Ala Tyr Leu Glu Leu Asp Pro
305 310 315 320
Arg Asp Phe Lys Val Thr Glu Glu Trp Gln Lys Glu Asn Leu Lys Ile

				325					330				335				
Arg	Ser	Lys	Ala	Gln	Ala	Lys	Met	Leu	Glu	Met	Arg	Asn	Pro	Gln	Ala		
			340					345					350				
His	Leu	Ser	Asn	Ser	Gln	Ser	Leu	Phe	Val	Gln	Lys	Ile	Phe	Ala			
		355					360					365					
Asp	Val	Asn	Lys	Glu	Ile	Glu	Ala	Val	Ala	Asn	Thr	Glu	Lys	Lys	Ala		
	370					375					380						
Glu	Lys	Ala	Gly	Tyr	Gly	Tyr	Ser	Lys	Arg	Met							
385					390					395							

<210> 75
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 <212> DNA
 <213> Helicobacter pylori

<220>
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 <222> (70)...(864)

<400> 75
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 aggttaaac atg att aaa caa acc ctc atc att ctt gcc cct ttt ttt atc 111
 Met Ile Lys Gln Thr Leu Ile Ile Leu Ala Pro Phe Phe Ile
 1 5 10

gca	acg	ctg	ttg	tat	ttt	tta	ggc	gca	ccg	gat	ggg	tta	aga	cct	aac	159
Ala	Thr	Leu	Leu	Tyr	Phe	Leu	Gly	Ala	Pro	Asp	Gly	Leu	Arg	Pro	Asn	
15					20					25					30	

gct	tgg	ctt	tat	ttt	tgt	att	ttc	atg	ggc	atg	att	ata	ggg	cta	att	207
Ala	Trp	Leu	Tyr	Phe	Cys	Ile	Phe	Met	Gly	Met	Ile	Ile	Gly	Leu	Ile	
				35					40					45		

tta	gag	ccg	gtg	cca	tca	ggg	tta	ata	gcg	cta	agc	gcg	tta	gtg	ctg	255
Leu	Glu	Pro	Val	Pro	Ser	Gly	Leu	Ile	Ala	Leu	Ser	Ala	Leu	Val	Leu	
			50						55					60		

tgt	ata	gcg	tta	aaa	att	gga	gcg	agc	gat	aaa	gta	gcg	agc	gct	aat	303
Cys	Ile	Ala	Leu	Lys	Ile	Gly	Ala	Ser	Asp	Lys	Val	Ala	Ser	Ala	Asn	
		65					70					75				

aag	gct	att	tcg	tgg	ggg	ttg	agc	ggg	tat	gcg	aat	aaa	acg	gtg	tgg	351
Lys	Ala	Ile	Ser	Trp	Gly	Leu	Ser	Gly	Tyr	Ala	Asn	Lys	Thr	Val	Trp	
	80					85					90					

ctt	gtg	ttt	gtc	gct	ttc	att	ttg	ggg	tta	ggg	tat	gaa	aaa	agc	ttg	399
Leu	Val	Phe	Val	Ala	Phe	Ile	Leu	Gly	Leu	Gly	Tyr	Glu	Lys	Ser	Leu	
	95					100				105					110	

tta	ggg	aaa	cgg	atc	gct	ctt	tta	ctg	att	agg	ttt	tta	ggg	caa	acc	447
Leu	Gly	Lys	Arg	Ile	Ala	Leu	Leu	Leu	Ile	Arg	Phe	Leu	Gly	Gln	Thr	
			115						120					125		

cct	tta	ggg	tta	ggc	tat	gcg	att	ggg	ttg	agc	gaa	ttg	tgt	cta	gcc	495
Pro	Leu	Gly	Leu	Gly	Tyr	Ala	Ile	Gly	Leu	Ser	Glu	Leu	Cys	Leu	Ala	
			130					135					140			

cct ttt atc cct agc aac tcc gct aga agt gga ggc ata ctc tat ccc	543
Pro Phe Ile Pro Ser Asn Ser Ala Arg Ser Gly Gly Ile Leu Tyr Pro	
145 150 155	
atc gtt tca tct atc ccg cct tta atg gga tct act cca aat aat aac	591
Ile Val Ser Ser Ile Pro Pro Leu Met Gly Ser Thr Pro Asn Asn Asn	
160 165 170	
cct gac aaa atc ggc gcg tat ttg atg tgg gtc gct ttg gct tca act	639
Pro Asp Lys Ile Gly Ala Tyr Leu Met Trp Val Ala Leu Ala Ser Thr	
175 180 185 190	
tgc atc act tcg tcc atg ttt tta acc gcg ctc gct cct aac ccc cta	687
Cys Ile Thr Ser Ser Met Phe Leu Thr Ala Leu Ala Pro Asn Pro Leu	
195 200 205	
gca atg gaa atc gct gcc aaa atg ggc gtg aat gaa atc tca tgg ttt	735
Ala Met Glu Ile Ala Ala Lys Met Gly Val Asn Glu Ile Ser Trp Phe	
210 215 220	
tcg tgg ttt tta gcg ttc ttg cct tgt ggg gtg gtt ttg atc ttg ctt	783
Ser Trp Phe Leu Ala Phe Leu Pro Cys Gly Val Val Leu Ile Leu Leu	
225 230 235	
gtg cct tta ttg gcg tat aaa acc tgc aaa ccc acc tta aaa ggc tca	831
Val Pro Leu Leu Ala Tyr Lys Thr Cys Lys Pro Thr Leu Lys Gly Ser	
240 245 250	
aaa gaa gtg agt ttg tgg gcc aaa aaa agg aat tagagggcat ggggaggttt	884
Lys Glu Val Ser Leu Trp Ala Lys Lys Arg Asn	
255 260 265	

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 <212> PRT
 <213> Helicobacter pylori

<400> 76

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Leu Leu Tyr Phe Leu Gly Ala Pro Asp Gly Leu Arg Pro Asn Ala Trp	
20 25 30	
Leu Tyr Phe Cys Ile Phe Met Gly Met Ile Ile Gly Leu Ile Leu Glu	
35 40 45	
Pro Val Pro Ser Gly Leu Ile Ala Leu Ser Ala Leu Val Leu Cys Ile	
50 55 60	
Ala Leu Lys Ile Gly Ala Ser Asp Lys Val Ala Ser Ala Asn Lys Ala	
65 70 75 80	
Ile Ser Trp Gly Leu Ser Gly Tyr Ala Asn Lys Thr Val Trp Leu Val	
85 90 95	
Phe Val Ala Phe Ile Leu Gly Leu Gly Tyr Glu Lys Ser Leu Leu Gly	
100 105 110	
Lys Arg Ile Ala Leu Leu Leu Ile Arg Phe Leu Gly Gln Thr Pro Leu	
115 120 125	
Gly Leu Gly Tyr Ala Ile Gly Leu Ser Glu Leu Cys Leu Ala Pro Phe	
130 135 140	

tct atg tat gaa gat ggc gat ggt gtg caa aaa aac ctt cca aag gct	508
Ser Met Tyr Glu Asp Gly Asp Gly Val Gln Lys Asn Leu Pro Lys Ala	
105 110 115	
atc tat tat tac agg aga ggg tgc cac tta aag ggt ggg gtg agc tgt	556
Ile Tyr Tyr Tyr Arg Arg Gly Cys His Leu Lys Gly Gly Val Ser Cys	
120 125 130 135	
ggg agt tta ggt ttt atg tat ttt aat ggc acg ggc gtt aag caa aat	604
Gly Ser Leu Gly Phe Met Tyr Phe Asn Gly Thr Gly Val Lys Gln Asn	
140 145 150	
tat gcc aaa gcc ctt ttt ctt tct aaa tac gct tgc agt ttg aat tac	652
Tyr Ala Lys Ser Ala Leu Phe Leu Ser Lys Tyr Ala Cys Ser Leu Asn Tyr	
155 160 165	
ggc att agt tgt aac ttt gta ggg tat atg tat agg aac gcc aaa ggc	700
Gly Ile Ser Cys Asn Phe Val Gly Tyr Met Tyr Arg Asn Ala Lys Gly	
170 175 180	
gta cag aag gat ttg aaa aaa gcc ctt gcg aat ttt aaa aga ggg tgc	748
Val Gln Lys Asp Leu Lys Lys Ala Leu Ala Asn Phe Lys Arg Gly Cys	
185 190 195	
cat ttg aaa gac gga gcg agt tgt gtg agc ttg gga tac atg tat gaa	796
His Leu Lys Asp Gly Ala Ser Cys Val Ser Leu Gly Tyr Met Tyr Glu	
200 205 210 215	
gtc ggt atg gat gtc aaa caa aat gga gag caa gcc ttg aat ctt tat	844
Val Gly Met Asp Val Lys Gln Asn Gly Glu Gln Ala Leu Asn Leu Tyr	
220 225 230	
aaa aag ggt tgt tat tta aaa agg ggg agc ggt tgt cat aat gtg gcg	892
Lys Lys Gly Cys Tyr Leu Lys Arg Gly Ser Gly Cys His Asn Val Ala	
235 240 245	
gtg atg tat tac acc ggt aag ggc gtt cca aag gat tta gat aaa gcc	940
Val Met Tyr Tyr Thr Gly Lys Gly Val Pro Lys Asp Leu Asp Lys Ala	
250 255 260	
att tcg tat tat aag aaa ggt tgc act cta ggc ttt agt ggt agc tgt	988
Ile Ser Tyr Tyr Lys Lys Gly Cys Thr Leu Gly Phe Ser Gly Ser Cys	
265 270 275	
aaa gtg tta gaa gaa gtg att ggc aag aag tct gat gat ttg caa gat	1036
Lys Val Leu Glu Glu Val Ile Gly Lys Lys Ser Asp Asp Leu Gln Asp	
280 285 290 295	
gac gcg caa aac gac acg caa gat gat atg caa taagttaaag cttatggact	1089
Asp Ala Gln Asn Asp Thr Gln Asp Asp Met Gln	
300 305	
aatgattaaa actcatctta tagaaatctt tctactctct tggtatcaaa tagggattaa	1149
gcgtctctat tgatgggtat tgagactaaa aatctgcaaa tctag	1194

<210> 78
 <211> 306
 <212> PRT

<213> Helicobacter pylori

<400> 78

Met Ile Lys Ser Trp Thr Lys Lys Trp Phe Leu Ile Leu Phe Leu Met
1 5 10 15
Ala Ser Cys Ser Ser Tyr Leu Val Ala Thr Thr Gly Glu Lys Tyr Phe
20 25 30
Lys Met Ala Thr Gln Ala Phe Lys Arg Gly Asp Tyr His Lys Ala Val
35 40 45
Ala Phe Tyr Lys Arg Ser Cys Asn Leu Arg Val Gly Val Gly Cys Thr
50 55 60
Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Asp Gln Asn Ile
65 70 75 80
Thr Lys Ala Val Phe Tyr Tyr Arg Arg Gly Cys Asn Leu Arg Asn His
85 90 95
Leu Ala Cys Ala Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val
100 105 110
Gln Lys Asn Leu Pro Lys Ala Ile Tyr Tyr Tyr Arg Arg Gly Cys His
115 120 125
Leu Lys Gly Gly Val Ser Cys Gly Ser Leu Gly Phe Met Tyr Phe Asn
130 135 140
Gly Thr Gly Val Lys Gln Asn Tyr Ala Lys Ala Leu Phe Leu Ser Lys
145 150 155 160
Tyr Ala Cys Ser Leu Asn Tyr Gly Ile Ser Cys Asn Phe Val Gly Tyr
165 170 175
Met Tyr Arg Asn Ala Lys Gly Val Gln Lys Asp Leu Lys Lys Ala Leu
180 185 190
Ala Asn Phe Lys Arg Gly Cys His Leu Lys Asp Gly Ala Ser Cys Val
195 200 205
Ser Leu Gly Tyr Met Tyr Glu Val Gly Met Asp Val Lys Gln Asn Gly
210 215 220
Glu Gln Ala Leu Asn Leu Tyr Lys Lys Gly Cys Tyr Leu Lys Arg Gly
225 230 235 240
Ser Gly Cys His Asn Val Ala Val Met Tyr Tyr Thr Gly Lys Gly Val
245 250 255
Pro Lys Asp Leu Asp Lys Ala Ile Ser Tyr Tyr Lys Lys Gly Cys Thr
260 265 270
Leu Gly Phe Ser Gly Ser Cys Lys Val Leu Glu Glu Val Ile Gly Lys
275 280 285
Lys Ser Asp Asp Leu Gln Asp Asp Ala Gln Asn Asp Thr Gln Asp Asp
290 295 300
Met Gln
305

<210> 79

<211> 1001

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (101)...(865)

<400> 79

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gcgatttttag gttaattttg agtttttagg agcagttttt atg caa caa gaa gag 115
Met Gln Gln Glu Glu

	1	5	
att ata gag ggt tat tat ggt gct agc aaa ggg ctt aaa aag agc ggt Ile Ile Glu Gly Tyr Tyr Gly Ala Ser Lys Gly Leu Lys Lys Ser Gly	10	15	20
163			
att tat gcc aag ctg gat ttt tta cag agc gct acg ggc ttg att tta Ile Tyr Ala Lys Leu Asp Phe Leu Gln Ser Ala Thr Gly Leu Ile Leu	25	30	35
211			
gcg ctc ttt atg ata gca cac atg ttt tta gtc tca agt atc ttg att Ala Leu Phe Met Ile Ala His Met Phe Leu Val Ser Ser Ile Leu Ile	40	45	50
259			
agc gat gaa gcc atg tat aaa gtg gcg aaa ttt ttt gaa ggg agc ttg Ser Asp Glu Ala Met Tyr Lys Val Ala Lys Phe Phe Glu Gly Ser Leu	55	60	65
307			
ttt tta aaa gcg ggc gag ccg gct att gtg agc gtg gtt gca gca ggg Phe Leu Lys Ala Gly Glu Pro Ala Ile Val Ser Val Val Ala Ala Gly	70	75	80
355			
att att ctt att tta gtc gcg cat gct ttt ttg gcg tta agg aaa ttc Ile Ile Leu Ile Leu Val Ala His Ala Phe Leu Ala Leu Arg Lys Phe	90	95	100
403			
cct atc aat tac agg caa tac aag gtt ttt aaa acc cat aag cat ttg Pro Ile Asn Tyr Arg Gln Tyr Lys Val Phe Lys Thr His Lys His Leu	105	110	115
451			
atg aaa cat ggc gat acg agc ttg tgg ttt att caa gcc ctc acc ggg Met Lys His Gly Asp Thr Ser Leu Trp Phe Ile Gln Ala Leu Thr Gly	120	125	130
499			
ttt gcg atg ttt ttc tta gcg agt atc cac tta ttt gtc atg ctc aca Phe Ala Met Phe Phe Leu Ala Ser Ile His Leu Phe Val Met Leu Thr	135	140	145
547			
gag cct gaa agt att ggg cct cat ggt tca agc tat cgt ttt gta acg Glu Pro Glu Ser Ile Gly Pro His Gly Ser Ser Tyr Arg Phe Val Thr	150	155	160
595			
caa aac ttt tgg ctt ttg tat att ttc tta ttg ttt gcc gta gaa ttg Gln Asn Phe Trp Leu Leu Tyr Ile Phe Leu Leu Phe Ala Val Glu Leu	170	175	180
643			
cat ggc tct att ggg ttg tat cgt tta gcg atc aaa tgg ggg tgg ttt His Gly Ser Ile Gly Leu Tyr Arg Leu Ala Ile Lys Trp Gly Trp Phe	185	190	195
691			
aaa aat gtg agc att caa ggt ttg aga aaa gtc aaa tgg gcg atg agc Lys Asn Val Ser Ile Gln Gly Leu Arg Lys Val Lys Trp Ala Met Ser	200	205	210
739			
gtg ttt ttt att gtt tta ggg ctt tgc acc tat ggg gct tac att aaa Val Phe Phe Ile Val Leu Gly Leu Cys Thr Tyr Gly Ala Tyr Ile Lys	215	220	225
787			

aaa ggt tta gaa aat aag gaa aat ggc att aaa acc atg caa gaa gcc 835
 Lys Gly Leu Glu Asn Lys Glu Asn Gly Ile Lys Thr Met Gln Glu Ala
 230 235 240 245

ata gaa gct gat ggg aaa ttc cac aaa gaa taagggtaga aaatgaaaat 885
 Ile Glu Ala Asp Gly Lys Phe His Lys Glu
 250 255

aacatattgt gatgcgctaa ttattggagg cggactagct ggggtaaggg ctagtatcgc 945
 atgcaaacaa aagggttttaa acaccatcgt ttttaagccta gtgcctgtca ggcggtt 1001

<210> 80
 <211> 255
 <212> PRT
 <213> Helicobacter pylori

<400> 80
 Met Gln Gln Glu Glu Ile Ile Glu Gly Tyr Tyr Gly Ala Ser Lys Gly
 1 5 10 15
 Leu Lys Lys Ser Gly Ile Tyr Ala Lys Leu Asp Phe Leu Gln Ser Ala
 20 25 30
 Thr Gly Leu Ile Leu Ala Leu Phe Met Ile Ala His Met Phe Leu Val
 35 40 45
 Ser Ser Ile Leu Ile Ser Asp Glu Ala Met Tyr Lys Val Ala Lys Phe
 50 55 60
 Phe Glu Gly Ser Leu Phe Leu Lys Ala Gly Glu Pro Ala Ile Val Ser
 65 70 75 80
 Val Val Ala Ala Gly Ile Ile Leu Ile Leu Val Ala His Ala Phe Leu
 85 90 95
 Ala Leu Arg Lys Phe Pro Ile Asn Tyr Arg Gln Tyr Lys Val Phe Lys
 100 105 110
 Thr His Lys His Leu Met Lys His Gly Asp Thr Ser Leu Trp Phe Ile
 115 120 125
 Gln Ala Leu Thr Gly Phe Ala Met Phe Phe Leu Ala Ser Ile His Leu
 130 135 140
 Phe Val Met Leu Thr Glu Pro Glu Ser Ile Gly Pro His Gly Ser Ser
 145 150 155 160
 Tyr Arg Phe Val Thr Gln Asn Phe Trp Leu Leu Tyr Ile Phe Leu Leu
 165 170 175
 Phe Ala Val Glu Leu His Gly Ser Ile Gly Leu Tyr Arg Leu Ala Ile
 180 185 190
 Lys Trp Gly Trp Phe Lys Asn Val Ser Ile Gln Gly Leu Arg Lys Val
 195 200 205
 Lys Trp Ala Met Ser Val Phe Phe Ile Val Leu Gly Leu Cys Thr Tyr
 210 215 220
 Gly Ala Tyr Ile Lys Lys Gly Leu Glu Asn Lys Glu Asn Gly Ile Lys
 225 230 235 240
 Thr Met Gln Glu Ala Ile Glu Ala Asp Gly Lys Phe His Lys Glu
 245 250 255

<210> 81
 <211> 975
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS

<222> (82)...(912)

<400> 81

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ttttaaaatt aaagaaaatt ttttttaaag attatcactc ttttttgata aagtaatcat 60
ttaaaattta gggagttttt t atg gaa gaa tca aca gcg ttt att ttg gct 111
                               Met Glu Glu Ser Thr Ala Phe Ile Leu Ala
                               1                               5                               10

ctt gtg ggg cta ttc acc ggc att acc gcc ggg ttt ttt ggt att ggt 159
Leu Val Gly Leu Phe Thr Gly Ile Thr Ala Gly Phe Phe Gly Ile Gly
                               15                               20                               25

ggg ggg gag att gtc gtc cct agc gcg att ttt gcc cat ttt agc tat 207
Gly Gly Glu Ile Val Val Pro Ser Ala Ile Phe Ala His Phe Ser Tyr
                               30                               35                               40

agc cat gcg gtg ggt att tcg ctc atg caa atg ctt ttt tct tca gtg 255
Ser His Ala Val Gly Ile Ser Leu Met Gln Met Leu Phe Ser Ser Val
                               45                               50                               55

gtc ggc tct atc atc aat tac aaa aag ggc tta ttg gat ttg aga gaa 303
Val Gly Ser Ile Ile Asn Tyr Lys Lys Gly Leu Leu Asp Leu Arg Glu
                               60                               65                               70

ggc tca ttt gcc gcg ctt gga ggg cta atg gga gcg att tta ggg agc 351
Gly Ser Phe Ala Ala Leu Gly Gly Leu Met Gly Ala Ile Leu Gly Ser
                               75                               80                               85                               90

ttt atc tta aaa atc att gac gat aaa att tta atg gcg gtg ttt gtg 399
Phe Ile Leu Lys Ile Ile Asp Asp Lys Ile Leu Met Ala Val Phe Val
                               95                               100                               105

gtg gtg gtg tgc tac acc ttt atc aaa tac gct ttt tct agc aac aag 447
Val Val Val Cys Tyr Thr Phe Ile Lys Tyr Ala Phe Ser Ser Asn Lys
                               110                               115                               120

aaa ccc aag cat ttt gaa gaa atg cat ttt gat ttg cat gcg aat aac 495
Lys Pro Lys His Phe Glu Glu Met His Phe Asp Leu His Ala Asn Asn
                               125                               130                               135

aaa acg ccc gaa aaa aag cgc gca atc cct ttt gtg tct atg gat aga 543
Lys Thr Pro Glu Lys Lys Arg Ala Ile Pro Phe Val Ser Met Asp Arg
                               140                               145                               150

acg cat ggg gtt ttg atg ctc gcc ggt ttt gtt acc ggc atc ttt tct 591
Thr His Gly Val Leu Met Leu Ala Gly Phe Val Thr Gly Ile Phe Ser
                               155                               160                               165                               170

atc cca cta ggc atg ggt gga ggg att tta atg gtg ccg ttt ttg ggc 639
Ile Pro Leu Gly Met Gly Gly Gly Ile Leu Met Val Pro Phe Leu Gly
                               175                               180                               185

tat ttt ttg aaa tac gat tct aaa aaa atc gtg cct ttg ggg cta ttt 687
Tyr Phe Leu Lys Tyr Asp Ser Lys Lys Ile Val Pro Leu Gly Leu Phe
                               190                               195                               200

ttt gtg gtg ttc gct tct tta tct ggg gtc atc tct ctt tat aac ggg 735
Phe Val Val Phe Ala Ser Leu Ser Gly Val Ile Ser Leu Tyr Asn Gly
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205	210	215	
agg gtt ctt gat aat ata agc gtt caa gcg ggg gtg att acc ggc att			783
Arg Val Leu Asp Asn Ile Ser Val Gln Ala Gly Val Ile Thr Gly Ile			
220	225	230	
gga gcg ttt tta ggc gtg ggc att ggc atc aag ctt atc gct ttg gct			831
Gly Ala Phe Leu Gly Val Gly Ile Gly Ile Lys Leu Ile Ala Leu Ala			
235	240	245	250
aat gaa aag gtg cat aaa atc ctg ttg ctc ctt att tat gct tta agc			879
Asn Glu Lys Val His Lys Ile Leu Leu Leu Leu Ile Tyr Ala Leu Ser			
255	260	265	
att tta gcg act tta cac aag ctc att atg ggg taaatctaaa aacgcttcta			932
Ile Leu Ala Thr Leu His Lys Leu Ile Met Gly			
270	275		
gggcattttt aaaattaata tcaaagagct ttcaccagca agc			975

<210> 82
 <211> 277
 <212> PRT
 <213> Helicobacter pylori

<400> 82

Met Glu Glu Ser Thr Ala Phe Ile Leu Ala Leu Val Gly Leu Phe Thr			
1	5	10	15
Gly Ile Thr Ala Gly Phe Phe Gly Ile Gly Gly Gly Glu Ile Val Val			
20	25	30	
Pro Ser Ala Ile Phe Ala His Phe Ser Tyr Ser His Ala Val Gly Ile			
35	40	45	
Ser Leu Met Gln Met Leu Phe Ser Ser Val Val Gly Ser Ile Ile Asn			
50	55	60	
Tyr Lys Lys Gly Leu Leu Asp Leu Arg Glu Gly Ser Phe Ala Ala Leu			
65	70	75	80
Gly Gly Leu Met Gly Ala Ile Leu Gly Ser Phe Ile Leu Lys Ile Ile			
85	90	95	
Asp Asp Lys Ile Leu Met Ala Val Phe Val Val Val Val Cys Tyr Thr			
100	105	110	
Phe Ile Lys Tyr Ala Phe Ser Ser Asn Lys Lys Pro Lys His Phe Glu			
115	120	125	
Glu Met His Phe Asp Leu His Ala Asn Asn Lys Thr Pro Glu Lys Lys			
130	135	140	
Arg Ala Ile Pro Phe Val Ser Met Asp Arg Thr His Gly Val Leu Met			
145	150	155	160
Leu Ala Gly Phe Val Thr Gly Ile Phe Ser Ile Pro Leu Gly Met Gly			
165	170	175	
Gly Gly Ile Leu Met Val Pro Phe Leu Gly Tyr Phe Leu Lys Tyr Asp			
180	185	190	
Ser Lys Lys Ile Val Pro Leu Gly Leu Phe Phe Val Val Phe Ala Ser			
195	200	205	
Leu Ser Gly Val Ile Ser Leu Tyr Asn Gly Arg Val Leu Asp Asn Ile			
210	215	220	
Ser Val Gln Ala Gly Val Ile Thr Gly Ile Gly Ala Phe Leu Gly Val			
225	230	235	240
Gly Ile Gly Ile Lys Leu Ile Ala Leu Ala Asn Glu Lys Val His Lys			
245	250	255	

Ile Leu Leu Leu Leu Ile Tyr Ala Leu Ser Ile Leu Ala Thr Leu His
 260 265 270
 Lys Leu Ile Met Gly
 275

<210> 83
 <211> 1667
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (220)...(1482)

<400> 83
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 aaggctcttg atgaaaaata ccaatacaaa agagataaag aatacaagaa tgaaaaaagg 120
 ttatagtcaa taccacgcgc tcaaaaaagg gcttttaaaa acgctctgct ttttagcctt 180
 cctttaagcg tggcggttagc tgaagacgat ggcttttat atg gga gtg ggc tat 234
 Met Gly Val Gly Tyr
 1 5
 caa atc ggc ggc gcg caa caa aat atc gat aac aaa ggc agc acc cta 282
 Gln Ile Gly Gly Ala Gln Gln Asn Ile Asp Asn Lys Gly Ser Thr Leu
 10 15 20
 agg aat aat gtc att aat aat ttc cgc caa gtg ggc gtg ggt atg gca 330
 Arg Asn Asn Val Ile Asn Asn Phe Arg Gln Val Gly Val Gly Met Ala
 25 30 35
 ggg ggt aat ggg ctt tta gcc tta gcg aca aac acg acc atg gac gct 378
 Gly Gly Asn Gly Leu Leu Ala Leu Ala Thr Asn Thr Thr Met Asp Ala
 40 45 50
 ctt tta ggg ata ggc aac caa att gtc aat act aat aca act gtt agc 426
 Leu Leu Gly Ile Gly Asn Gln Ile Val Asn Thr Asn Thr Thr Val Ser
 55 60 65
 aac aac aac gca gaa tta acc cag ttt aaa aaa ata ctc cct caa att 474
 Asn Asn Asn Ala Glu Leu Thr Gln Phe Lys Lys Ile Leu Pro Gln Ile
 70 75 80 85
 gag caa cgc ttt gaa acg aat aaa aac gct tat agc gtt caa gcc ttg 522
 Glu Gln Arg Phe Glu Thr Asn Lys Asn Ala Tyr Ser Val Gln Ala Leu
 90 95 100
 caa gtg tat ttg agt aat gtg ctt tat aac ttg gtt aat aat agt aat 570
 Gln Val Tyr Leu Ser Asn Val Leu Tyr Asn Leu Val Asn Asn Ser Asn
 105 110 115
 aat ggc agt aat aat gga gtc gtt cct gaa tat gta gga att ata aaa 618
 Asn Gly Ser Asn Asn Gly Val Val Pro Glu Tyr Val Gly Ile Ile Lys
 120 125 130
 gtt ctc tat ggt tct caa aat gaa ttc agt ctc tta gcc acg gag agt 666
 Val Leu Tyr Gly Ser Gln Asn Glu Phe Ser Leu Leu Ala Thr Glu Ser
 135 140 145

gtg	gtg	ctt	tta	aac	gcg	ctt	aca	agg	gtg	aat	ctg	gat	agt	aat	tcg	714
Val	Val	Leu	Leu	Asn	Ala	Leu	Thr	Arg	Val	Asn	Leu	Asp	Ser	Asn	Ser	
150					155				160						165	
gtg	ttt	tta	aaa	ggg	cta	tta	gcc	caa	atg	cag	ctt	ttt	aat	gac	act	762
Val	Phe	Leu	Lys	Gly	Leu	Leu	Ala	Gln	Met	Gln	Leu	Phe	Asn	Asp	Thr	
				170					175						180	
tct	tca	gca	aag	cta	ggc	cag	atc	gca	gaa	aac	ttg	aag	aac	ggg	ggg	810
Ser	Ser	Ala	Lys	Leu	Gly	Gln	Ile	Ala	Glu	Asn	Leu	Lys	Asn	Gly	Gly	
			185					190						195		
gca	gga	tca	atg	ctc	caa	aag	gat	gtg	aaa	acc	atc	tcg	gat	cga	atc	858
Ala	Gly	Ser	Met	Leu	Gln	Lys	Asp	Val	Lys	Thr	Ile	Ser	Asp	Arg	Ile	
			200				205							210		
gct	act	tac	caa	gag	aat	cta	aaa	cag	cta	gga	ggg	atg	cta	aag	aat	906
Ala	Thr	Tyr	Gln	Glu	Asn	Leu	Lys	Gln	Leu	Gly	Gly	Met	Leu	Lys	Asn	
	215					220					225					
tac	gat	gaa	ccc	tac	ttg	ccc	caa	ttt	ggg	cca	ggc	aca	agc	tct	cag	954
Tyr	Asp	Glu	Pro	Tyr	Leu	Pro	Gln	Phe	Gly	Pro	Gly	Thr	Ser	Ser	Gln	
230					235					240					245	
cat	ggg	gtt	att	aat	ggc	ttt	ggc	att	caa	gtg	ggc	tat	aag	caa	ttt	1002
His	Gly	Val	Ile	Asn	Gly	Phe	Gly	Ile	Gln	Val	Gly	Tyr	Lys	Gln	Phe	
				250					255						260	
ttt	ggg	aac	aag	cgg	aat	ata	ggc	tta	cga	tat	tac	gct	ttc	ttt	gat	1050
Phe	Gly	Asn	Lys	Arg	Asn	Ile	Gly	Leu	Arg	Tyr	Tyr	Ala	Phe	Phe	Asp	
			265					270						275		
tat	ggc	ttt	acg	caa	ttg	ggc	agt	ctt	agc	agc	gcc	gtt	aaa	gcg	aat	1098
Tyr	Gly	Phe	Thr	Gln	Leu	Gly	Ser	Leu	Ser	Ser	Ala	Val	Lys	Ala	Asn	
			280				285							290		
atc	ttt	act	tat	ggc	gct	ggc	acg	gac	ttt	tta	tgg	aat	atc	ttt	aga	1146
Ile	Phe	Thr	Tyr	Gly	Ala	Gly	Thr	Asp	Phe	Leu	Trp	Asn	Ile	Phe	Arg	
	295					300					305					
agg	gtt	ttt	agc	gat	cag	tcc	ttg	aat	gtg	ggg	gtg	ttt	ggg	ggc	att	1194
Arg	Val	Phe	Ser	Asp	Gln	Ser	Leu	Asn	Val	Gly	Val	Phe	Gly	Gly	Ile	
310					315					320					325	
caa	ata	gcg	ggg	aac	act	tgg	gat	agc	tct	tta	aga	ggg	caa	att	gaa	1242
Gln	Ile	Ala	Gly	Asn	Thr	Trp	Asp	Ser	Ser	Leu	Arg	Gly	Gln	Ile	Glu	
				330					335						340	
aac	tcg	ttt	aaa	gaa	tac	ccc	act	ccc	acg	aat	ttc	caa	ttt	ttg	ttt	1290
Asn	Ser	Phe	Lys	Glu	Tyr	Pro	Thr	Pro	Thr	Asn	Phe	Gln	Phe	Leu	Phe	
			345					350						355		
aat	ttg	ggg	tta	agg	gct	cat	ttt	gcc	agc	acc	atg	cac	cgc	cgg	ttt	1338
Asn	Leu	Gly	Leu	Arg	Ala	His	Phe	Ala	Ser	Thr	Met	His	Arg	Arg	Phe	
			360				365					370				
ttg	agc	gcg	tct	caa	agc	att	cag	cat	ggg	atg	gaa	ttt	ggc	gtg	aaa	1386

Leu Ser Ala Ser Gln Ser Ile Gln His Gly Met Glu Phe Gly Val Lys
 375 380 385

atc ccg gct atc aat caa agg tat ttg agg gcc aat ggg gct gat gtg 1434
 Ile Pro Ala Ile Asn Gln Arg Tyr Leu Arg Ala Asn Gly Ala Asp Val
 390 395 400 405

gat tac agg cgt ttg tat gcg ttc tat atc aat tac acg ata ggt ttt 1482
 Asp Tyr Arg Arg Leu Tyr Ala Phe Tyr Ile Asn Tyr Thr Ile Gly Phe
 410 415 420

taagctcttt ttagggctta taaagaggct ttttactttt tttttggtat tctaacaagc 1542
 ttttaaataa tccaatctac tttgttttaa ggataatatt ttatggcaga tgctgttg 1602
 gggatccagt ggggagatga ggggaaggga aaaattgttg ataggatcgc taaagattat 1662
 gactt 1667

<210> 84

<211> 421

<212> PRT

<213> Helicobacter pylori

<400> 84

Met Gly Val Gly Tyr Gln Ile Gly Gly Ala Gln Gln Asn Ile Asp Asn
 1 5 10 15
 Lys Gly Ser Thr Leu Arg Asn Asn Val Ile Asn Asn Phe Arg Gln Val
 20 25 30
 Gly Val Gly Met Ala Gly Gly Asn Gly Leu Leu Ala Leu Ala Thr Asn
 35 40 45
 Thr Thr Met Asp Ala Leu Leu Gly Ile Gly Asn Gln Ile Val Asn Thr
 50 55 60
 Asn Thr Thr Val Ser Asn Asn Ala Glu Leu Thr Gln Phe Lys Lys
 65 70 75 80
 Ile Leu Pro Gln Ile Glu Gln Arg Phe Glu Thr Asn Lys Asn Ala Tyr
 85 90 95
 Ser Val Gln Ala Leu Gln Val Tyr Leu Ser Asn Val Leu Tyr Asn Leu
 100 105 110
 Val Asn Asn Ser Asn Asn Gly Ser Asn Asn Gly Val Val Pro Glu Tyr
 115 120 125
 Val Gly Ile Ile Lys Val Leu Tyr Gly Ser Gln Asn Glu Phe Ser Leu
 130 135 140
 Leu Ala Thr Glu Ser Val Val Leu Leu Asn Ala Leu Thr Arg Val Asn
 145 150 155 160
 Leu Asp Ser Asn Ser Val Phe Leu Lys Gly Leu Leu Ala Gln Met Gln
 165 170 175
 Leu Phe Asn Asp Thr Ser Ser Ala Lys Leu Gly Gln Ile Ala Glu Asn
 180 185 190
 Leu Lys Asn Gly Gly Ala Gly Ser Met Leu Gln Lys Asp Val Lys Thr
 195 200 205
 Ile Ser Asp Arg Ile Ala Thr Tyr Gln Glu Asn Leu Lys Gln Leu Gly
 210 215 220
 Gly Met Leu Lys Asn Tyr Asp Glu Pro Tyr Leu Pro Gln Phe Gly Pro
 225 230 235 240
 Gly Thr Ser Ser Gln His Gly Val Ile Asn Gly Phe Gly Ile Gln Val
 245 250 255
 Gly Tyr Lys Gln Phe Phe Gly Asn Lys Arg Asn Ile Gly Leu Arg Tyr
 260 265 270
 Tyr Ala Phe Phe Asp Tyr Gly Phe Thr Gln Leu Gly Ser Leu Ser Ser
 275 280 285

Ala	Val	Lys	Ala	Asn	Ile	Phe	Thr	Tyr	Gly	Ala	Gly	Thr	Asp	Phe	Leu
290						295					300				
Trp	Asn	Ile	Phe	Arg	Arg	Val	Phe	Ser	Asp	Gln	Ser	Leu	Asn	Val	Gly
305					310					315					320
Val	Phe	Gly	Gly	Ile	Gln	Ile	Ala	Gly	Asn	Thr	Trp	Asp	Ser	Ser	Leu
				325					330					335	
Arg	Gly	Gln	Ile	Glu	Asn	Ser	Phe	Lys	Glu	Tyr	Pro	Thr	Pro	Thr	Asn
			340					345					350		
Phe	Gln	Phe	Leu	Phe	Asn	Leu	Gly	Leu	Arg	Ala	His	Phe	Ala	Ser	Thr
		355					360					365			
Met	His	Arg	Arg	Phe	Leu	Ser	Ala	Ser	Gln	Ser	Ile	Gln	His	Gly	Met
	370					375					380				
Glu	Phe	Gly	Val	Lys	Ile	Pro	Ala	Ile	Asn	Gln	Arg	Tyr	Leu	Arg	Ala
385					390					395					400
Asn	Gly	Ala	Asp	Val	Asp	Tyr	Arg	Arg	Leu	Tyr	Ala	Phe	Tyr	Ile	Asn
			405						410					415	
Tyr	Thr	Ile	Gly	Phe											
			420												

<210> 85
 <211> 926
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (207)...(746)

<400> 85
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 agactttgta gaaaaagtgg ttgttttaga cagctgtcaa atccaccaa aagcgtaat 120
 gcatttgcaa gaaactttga tgatagaagt ggataggctt gatttttctt tagtggagcg 180
 cttgaacatt ttagcgcgca tggaga atg aaa agc atg cgt ttt agt tac att 233
 Met Lys Ser Met Arg Phe Ser Tyr Ile
 1 5

gag cca aga gcg aaa tac ctt atc agc aag ctt tct aaa att tgg gtt 281
 Glu Pro Arg Ala Lys Tyr Leu Ile Ser Lys Leu Ser Lys Ile Trp Val
 10 15 20 25

ttt tac att ttt tta tct ttt gtg gta ata ggg ggg tta gtg tgg ttt 329
 Phe Tyr Ile Phe Leu Ser Phe Val Val Ile Gly Gly Leu Val Trp Phe
 30 35 40

atg cac aac gcc att aaa agc act caa gac aac gcg tcc agt ttg acg 377
 Met His Asn Ala Ile Lys Ser Thr Gln Asp Asn Ala Ser Ser Leu Thr
 45 50 55

atc caa gaa agg ctc tac cgc cat gaa atc agc cgc tta cag gtt aag 425
 Ile Gln Glu Arg Leu Tyr Arg His Glu Ile Ser Arg Leu Gln Val Lys
 60 65 70

act gat gaa acc tta aaa ctc att aaa gaa gcc aaa aag cgt ttg aat 473
 Thr Asp Glu Thr Leu Lys Leu Ile Lys Glu Ala Lys Lys Arg Leu Asn
 75 80 85

tat aac gat gat ata cga gat gtt ttg caa ggg ctt ttg aat att gtg 521

Tyr Asn Asp Asp Ile Arg Asp Val Leu Gln Gly Leu Leu Asn Ile Val
 90 95 100 105
 ccg gat tcc atc act att aat agc att gaa ata gac cag caa agc gtg 569
 Pro Asp Ser Ile Thr Ile Asn Ser Ile Glu Ile Asp Gln Gln Ser Val
 110 115 120
 gtt gtt agc ggt aaa acc cct tct aaa gaa gcc ttt tat ttt ttg ttt 617
 Val Val Ser Gly Lys Thr Pro Ser Lys Glu Ala Phe Tyr Phe Leu Phe
 125 130 135
 caa aac aaa cta aac ccc atg ttt gat tat tct agg gcg gaa ttt ttc 665
 Gln Asn Lys Leu Asn Pro Met Phe Asp Tyr Ser Arg Ala Glu Phe Phe
 140 145 150
 ccc tta agc gat ggg tgg ttt aat ttt gtc tcc acc aac ttt tct aat 713
 Pro Leu Ser Asp Gly Trp Phe Asn Phe Val Ser Thr Asn Phe Ser Asn
 155 160 165
 tcc tta ctg ata aaa aat ccg gag tct att aaa tgaagccatt gcattttttca 766
 Ser Leu Leu Ile Lys Asn Pro Glu Ser Ile Lys
 170 175 180
 cacctggaca gagagcaatc aggcgatgtg ggggtttatca ttaaaaacct cgtttttttta 826
 ggggtttttt ccttattggg ttggttgaat accgagtatt ttctatggcc tagcatgctg 886
 gaattaaaaa aaatcctttt agaagaaaat cgtaaaaaaa 926

<210> 86
 <211> 180
 <212> PRT
 <213> Helicobacter pylori

<400> 86
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 20 25 30
 Val Val Ile Gly Gly Leu Val Trp Phe Met His Asn Ala Ile Lys Ser
 35 40 45
 Thr Gln Asp Asn Ala Ser Ser Leu Thr Ile Gln Glu Arg Leu Tyr Arg
 50 55 60
 His Glu Ile Ser Arg Leu Gln Val Lys Thr Asp Glu Thr Leu Lys Leu
 65 70 75 80
 Ile Lys Glu Ala Lys Lys Arg Leu Asn Tyr Asn Asp Asp Ile Arg Asp
 85 90 95
 Val Leu Gln Gly Leu Leu Asn Ile Val Pro Asp Ser Ile Thr Ile Asn
 100 105 110
 Ser Ile Glu Ile Asp Gln Gln Ser Val Val Val Ser Gly Lys Thr Pro
 115 120 125
 Ser Lys Glu Ala Phe Tyr Phe Leu Phe Gln Asn Lys Leu Asn Pro Met
 130 135 140
 Phe Asp Tyr Ser Arg Ala Glu Phe Phe Pro Leu Ser Asp Gly Trp Phe
 145 150 155 160
 Asn Phe Val Ser Thr Asn Phe Ser Asn Ser Leu Leu Ile Lys Asn Pro
 165 170 175
 Glu Ser Ile Lys
 180

<210> 87
 <211> 1440
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (151)...(1299)

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 cataaaatca ttcaaaccce tttcaaacgc atg tgc gtg gtt ttg agc gtg aaa 174
 Met Cys Val Val Leu Ser Val Lys
 1 5

aga gat ggt gaa aaa act tta gaa aat aat gaa gaa aat aaa gat gaa 222
 Arg Asp Gly Glu Lys Thr Leu Glu Asn Asn Glu Glu Asn Lys Asp Glu
 10 15 20

aag ctt att ttg att gat gaa ttt gaa gtt tta gcc aat aaa ttc att 270
 Lys Leu Ile Leu Ile Asp Glu Phe Glu Val Leu Ala Asn Lys Phe Ile
 25 30 35 40

tct cgt ttg ccc aat atc cct agc acc cct aga gag ttt ggg tta ggc 318
 Ser Arg Leu Pro Asn Ile Pro Ser Thr Pro Arg Glu Phe Gly Leu Gly
 45 50 55

aag ggc gag atc atg gag att gat gtg cct ttt ggg agt att ttt gct 366
 Lys Gly Glu Ile Met Glu Ile Asp Val Pro Phe Gly Ser Ile Phe Ala
 60 65 70

tac aga cac att ggc tct atc aga caa aaa gaa tac agg att gta ggg 414
 Tyr Arg His Ile Gly Ser Ile Arg Gln Lys Glu Tyr Arg Ile Val Gly
 75 80 85

ctt tat cgc aac gat gtt ttg ttg ctc tcc act aaa tct tta gtt atc 462
 Leu Tyr Arg Asn Asp Val Leu Leu Leu Ser Thr Lys Ser Leu Val Ile
 90 95 100

cag ccg cga gac att ctc tta gtg gcg ggt aat ccg gaa att ttg aat 510
 Gln Pro Arg Asp Ile Leu Leu Val Ala Gly Asn Pro Glu Ile Leu Asn
 105 110 115 120

gcg gtg tat ctt caa gtc aaa agc aat gtg ggg cag ttc cca gcc ccc 558
 Ala Val Tyr Leu Gln Val Lys Ser Asn Val Gly Gln Phe Pro Ala Pro
 125 130 135

ttt ggt aag agc att tat tta tac att gat atg cgt ttg cag aac aga 606
 Phe Gly Lys Ser Ile Tyr Leu Tyr Ile Asp Met Arg Leu Gln Asn Arg
 140 145 150

aaa gcg atg atg cgc gat gtg tat caa gcc ttg ttt ttg cac aaa cat 654
 Lys Ala Met Met Arg Asp Val Tyr Gln Ala Leu Phe Leu His Lys His
 155 160 165

tta aag agc tac aag ctc tac att cag gtt tta cac ccc act agc cct 702
 Leu Lys Ser Tyr Lys Leu Tyr Ile Gln Val Leu His Pro Thr Ser Pro

170	175	180	
aag ttt tac cat aaa ttt tta gcg cta gaa acc gaa agc att gaa gtg Lys Phe Tyr His Lys Phe Leu Ala Leu Glu Thr Glu Ser Ile Glu Val 185 190 195 200			750
aat ttt gat ttt tac agg aaa agt ttt atc caa aaa ctc cat gaa gac Asn Phe Asp Phe Tyr Arg Lys Ser Phe Ile Gln Lys Leu His Glu Asp 205 210 215			798
cac cag aaa aaa atg ggc cta atc gtg gta ggc aga gag ctt ttt tta His Gln Lys Lys Met Gly Leu Ile Val Val Gly Arg Glu Leu Phe Leu 220 225 230			846
tct aaa aaa cac cga aag gcc ttg tat aaa aca gcc acc cca gtt tat Ser Lys Lys His Arg Lys Ala Leu Tyr Lys Thr Ala Thr Pro Val Tyr 235 240 245			894
aaa acc aac act tct ggc ttg tct aaa acc tct caa agc gtg gtg gta Lys Thr Asn Thr Ser Gly Leu Ser Lys Thr Ser Gln Ser Val Val Val 250 255 260			942
ttg aat gaa agt ttg gat att aat gag gac atg tct tca gtg att ttt Leu Asn Glu Ser Leu Asp Ile Asn Glu Asp Met Ser Ser Val Ile Phe 265 270 275 280			990
gat gtg tct atg caa atg gat ttg ggc ttg ttg ctc tat gat ttt gac Asp Val Ser Met Gln Met Asp Leu Gly Leu Leu Leu Tyr Asp Phe Asp 285 290 295			1038
cct aac aag cgc tat aaa aac gag att gtc aat cat tat gaa aat tta Pro Asn Lys Arg Tyr Lys Asn Glu Ile Val Asn His Tyr Glu Asn Leu 300 305 310			1086
gcc aac gcg ttc aac cgc aag att gag att ttc caa acc gat att aga Ala Asn Ala Phe Asn Arg Lys Ile Glu Ile Phe Gln Thr Asp Ile Arg 315 320 325			1134
aat cct atc atg tat ctc aat tct tta aga aat ccc att ttg cat ttc Asn Pro Ile Met Tyr Leu Asn Ser Leu Arg Asn Pro Ile Leu His Phe 330 335 340			1182
atg cct ttt gaa gag tgc atc acg cac acg cgc ttt tgg tgg ttt tta Met Pro Phe Glu Glu Cys Ile Thr His Thr Arg Phe Trp Trp Phe Leu 345 350 355 360			1230
tcc act aaa gtg gaa aaa tta gcg ttt tta aac gat gat aac cct caa Ser Thr Lys Val Glu Lys Leu Ala Phe Leu Asn Asp Asp Asn Pro Gln 365 370 375			1278
att ttt atc cct gta gcg gag tgaaagaatg caagaaattt taatcccttt Ile Phe Ile Pro Val Ala Glu 380			1329
aaaagaaaaa aactataaaag tggtttttggg ggaactgcct gaaataaaaat tgaaacaaaa agccctcatc attagcgata gcatcgtagc cgggttgcatt ttgccctatt t			1389 1440

<210> 88

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Asn	Asn	Glu	Glu	Asn	Lys	Asp	Glu	Lys	Leu	Ile	Leu	Ile	Asp	Glu	Phe
			20					25					30		
Glu	Val	Leu	Ala	Asn	Lys	Phe	Ile	Ser	Arg	Leu	Pro	Asn	Ile	Pro	Ser
		35					40					45			
Thr	Pro	Arg	Glu	Phe	Gly	Leu	Gly	Lys	Gly	Glu	Ile	Met	Glu	Ile	Asp
	50				55						60				
Val	Pro	Phe	Gly	Ser	Ile	Phe	Ala	Tyr	Arg	His	Ile	Gly	Ser	Ile	Arg
65					70					75					80
Gln	Lys	Glu	Tyr	Arg	Ile	Val	Gly	Leu	Tyr	Arg	Asn	Asp	Val	Leu	Leu
				85					90					95	
Leu	Ser	Thr	Lys	Ser	Leu	Val	Ile	Gln	Pro	Arg	Asp	Ile	Leu	Leu	Val
			100					105				110			
Ala	Gly	Asn	Pro	Glu	Ile	Leu	Asn	Ala	Val	Tyr	Leu	Gln	Val	Lys	Ser
		115					120					125			
Asn	Val	Gly	Gln	Phe	Pro	Ala	Pro	Phe	Gly	Lys	Ser	Ile	Tyr	Leu	Tyr
	130					135					140				
Ile	Asp	Met	Arg	Leu	Gln	Asn	Arg	Lys	Ala	Met	Met	Arg	Asp	Val	Tyr
145					150					155					160
Gln	Ala	Leu	Phe	Leu	His	Lys	His	Leu	Lys	Ser	Tyr	Lys	Leu	Tyr	Ile
				165					170					175	
Gln	Val	Leu	His	Pro	Thr	Ser	Pro	Lys	Phe	Tyr	His	Lys	Phe	Leu	Ala
			180					185					190		
Leu	Glu	Thr	Glu	Ser	Ile	Glu	Val	Asn	Phe	Asp	Phe	Tyr	Arg	Lys	Ser
		195					200					205			
Phe	Ile	Gln	Lys	Leu	His	Glu	Asp	His	Gln	Lys	Lys	Met	Gly	Leu	Ile
	210					215					220				
Val	Val	Gly	Arg	Glu	Leu	Phe	Leu	Ser	Lys	Lys	His	Arg	Lys	Ala	Leu
225					230					235					240
Tyr	Lys	Thr	Ala	Thr	Pro	Val	Tyr	Lys	Thr	Asn	Thr	Ser	Gly	Leu	Ser
				245					250					255	
Lys	Thr	Ser	Gln	Ser	Val	Val	Val	Leu	Asn	Glu	Ser	Leu	Asp	Ile	Asn
			260					265					270		
Glu	Asp	Met	Ser	Ser	Val	Ile	Phe	Asp	Val	Ser	Met	Gln	Met	Asp	Leu
		275					280					285			
Gly	Leu	Leu	Leu	Tyr	Asp	Phe	Asp	Pro	Asn	Lys	Arg	Tyr	Lys	Asn	Glu
	290					295					300				
Ile	Val	Asn	His	Tyr	Glu	Asn	Leu	Ala	Asn	Ala	Phe	Asn	Arg	Lys	Ile
305					310					315					320
Glu	Ile	Phe	Gln	Thr	Asp	Ile	Arg	Asn	Pro	Ile	Met	Tyr	Leu	Asn	Ser
				325					330					335	
Leu	Arg	Asn	Pro	Ile	Leu	His	Phe	Met	Pro	Phe	Glu	Glu	Cys	Ile	Thr
			340				345						350		
His	Thr														

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<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(464)

<400> 89

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agatttcatt cgaggtagaa aatacattga aaaagcgtgt gaattaaacg atg gta      56
                                     Met Val
                                     1

ggg ggt gga acg gta aaa aaa gac ttg aag aaa gcc att caa tac tat      104
Gly Gly Gly Thr Val Lys Lys Asp Leu Lys Lys Ala Ile Gln Tyr Tyr
      5                               10                               15

gtt aaa gcg tgt gaa ttg aat gaa atg ttt ggg tgt ctg tca tta gtt      152
Val Lys Ala Cys Glu Leu Asn Glu Met Phe Gly Cys Leu Ser Leu Val
      20                               25                               30

tcg aac tct caa ata aac aaa caa aaa ctc ttt caa tat ctc tct aaa      200
Ser Asn Ser Gln Ile Asn Lys Gln Lys Leu Phe Gln Tyr Leu Ser Lys
      35                               40                               45                               50

gct tgt gaa tta aat agt ggt aat gga tgt agg ttt tta ggg gat ttt      248
Ala Cys Glu Leu Asn Ser Gly Asn Gly Cys Arg Phe Leu Gly Asp Phe
      55                               60                               65

tat gag aat gga aaa tat gta aaa aag gat tta aga aaa gct gct caa      296
Tyr Glu Asn Gly Lys Tyr Val Lys Lys Asp Leu Arg Lys Ala Ala Gln
      70                               75                               80

tac tac tct aaa gct tgt gga tta aat gat caa gat ggg tgt tta ata      344
Tyr Tyr Ser Lys Ala Cys Gly Leu Asn Asp Gln Asp Gly Cys Leu Ile
      85                               90                               95

cta gga tat aag caa tat gct ggc aag ggc gta gtc aaa aat gaa aaa      392
Leu Gly Tyr Lys Gln Tyr Ala Gly Lys Gly Val Val Lys Asn Glu Lys
      100                               105                               110

caa gcg gtg aaa acc ttt gaa aag gct tgt agg tta gga tct gaa gac      440
Gln Ala Val Lys Thr Phe Glu Lys Ala Cys Arg Leu Gly Ser Glu Asp
      115                               120                               125                               130

gca tgt ggt att tta aac aac tac tagatttgaa ataaatgctg ttttttagct      494
Ala Cys Gly Ile Leu Asn Asn Tyr
      135

ggctttcatg tttttgtaac ccc      517
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<210> 90

<211> 138

<212> PRT

<213> Helicobacter pylori

<400> 90

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Met Val Gly Gly Gly Thr Val Lys Lys Asp Leu Lys Lys Ala Ile Gln
 1      5      10      15
Tyr Tyr Val Lys Ala Cys Glu Leu Asn Glu Met Phe Gly Cys Leu Ser
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		20					25				30				
Leu	Val	Ser	Asn	Ser	Gln	Ile	Asn	Lys	Gln	Lys	Leu	Phe	Gln	Tyr	Leu
		35					40				45				
Ser	Lys	Ala	Cys	Glu	Leu	Asn	Ser	Gly	Asn	Gly	Cys	Arg	Phe	Leu	Gly
	50					55					60				
Asp	Phe	Tyr	Glu	Asn	Gly	Lys	Tyr	Val	Lys	Lys	Asp	Leu	Arg	Lys	Ala
65					70					75					80
Ala	Gln	Tyr	Tyr	Ser	Lys	Ala	Cys	Gly	Leu	Asn	Asp	Gln	Asp	Gly	Cys
				85					90					95	
Leu	Ile	Leu	Gly	Tyr	Lys	Gln	Tyr	Ala	Gly	Lys	Gly	Val	Val	Lys	Asn
			100					105					110		
Glu	Lys	Gln	Ala	Val	Lys	Thr	Phe	Glu	Lys	Ala	Cys	Arg	Leu	Gly	Ser
	115						120					125			
Glu	Asp	Ala	Cys	Gly	Ile	Leu	Asn	Asn	Tyr						
	130					135									

<210> 91
 <211> 1663
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (68)...(1600)

<400> 91
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 aacaaac atg aaa aaa ctt ctt tat acc ata ctc gcg ctt ctt tta atc 109
 Met Lys Lys Leu Leu Tyr Thr Ile Leu Ala Leu Leu Leu Ile
 1 5 10

ggc ctt tta aca atc tat ctc atc ctt ttt aca gaa tgg ggg aat aag 157
 Gly Leu Leu Thr Ile Tyr Leu Ile Leu Phe Thr Glu Trp Gly Asn Lys
 15 20 25 30

atc atc gct tcg tat ata gag aaa aaa atc aac ccg aac gag cac tac 205
 Ile Ile Ala Ser Tyr Ile Glu Lys Lys Ile Asn Pro Asn Glu His Tyr
 35 40 45

ttg agc gtt aaa acc ttt aaa ttg aga ttc aac tct ttg gat ttt aaa 253
 Leu Ser Val Lys Thr Phe Lys Leu Arg Phe Asn Ser Leu Asp Phe Lys
 50 55 60

gct caa gcc aac gat gat tcc acg ctc att ctt aag ggg gat ttt tca 301
 Ala Gln Ala Asn Asp Asp Ser Thr Leu Ile Leu Lys Gly Asp Phe Ser
 65 70 75

ctt tta aag caa agc gta aat ttg aat tac cat ata gat att aaa gat 349
 Leu Leu Lys Gln Ser Val Asn Leu Asn Tyr His Ile Asp Ile Lys Asp
 80 85 90

tta cgc tct ttc aaa gaa tgg ata ccc tac cct tta agg ggg gct gtt 397
 Leu Arg Ser Phe Lys Glu Trp Ile Pro Tyr Pro Leu Arg Gly Ala Val
 95 100 105 110

atc act tct ggg aat att aaa ggg cat aga aaa gcc ctt atg att caa 445
 Ile Thr Ser Gly Asn Ile Lys Gly His Arg Lys Ala Leu Met Ile Gln

115										120					125					
ggc gtc tct aat gtg gct caa tcc cac act gcc tac aat gcc ctt tta	493																			
Gly Val Ser Asn Val Ala Gln Ser His Thr Ala Tyr Asn Ala Leu Leu																				
130 135 140																				
gat gat ttc aag ctt tct cgc tta aat ttg aac gca caa gac gcc aat	541																			
Asp Asp Phe Lys Leu Ser Arg Leu Asn Leu Asn Ala Gln Asp Ala Asn																				
145 150 155																				
tta gaa gat ttg ctt tat tta atc aat cgc ccc gct tat gcg aac gca	589																			
Leu Glu Asp Leu Leu Tyr Leu Ile Asn Arg Pro Ala Tyr Ala Asn Ala																				
160 165 170																				
aaa gtg tcc tta cag gcg gat ttt aac tct cta aag cct tta gag ggg	637																			
Lys Val Ser Leu Gln Ala Asp Phe Asn Ser Leu Lys Pro Leu Glu Gly																				
175 180 185 190																				
cat ttg atc cta aca gct aat aac gct tta atc aat aac gcc cta atc	685																			
His Leu Ile Leu Thr Ala Asn Asn Ala Leu Ile Asn Asn Ala Leu Ile																				
195 200 205																				
aat caa att ttt cat tta aac ctt aaa gac acg ctt gtt ttc agc ctc	733																			
Asn Gln Ile Phe His Leu Asn Leu Lys Asp Thr Leu Val Phe Ser Leu																				
210 215 220																				
tcg cat tca agc gac ttt aaa gga aac aaa gcc atc agc gat acc acc	781																			
Ser His Ser Ser Asp Phe Lys Gly Asn Lys Ala Ile Ser Asp Thr Thr																				
225 230 235																				
ctg act agc cct tta gcc aat ttc aaa gcc cta aaa agc gaa tac ctt	829																			
Leu Thr Ser Pro Leu Ala Asn Phe Lys Ala Leu Lys Ser Glu Tyr Leu																				
240 245 250																				
ttc tct att tta aaa ctc aac gcc ccc tac act tta gaa atc ccc aat	877																			
Phe Ser Ile Leu Lys Leu Asn Ala Pro Tyr Thr Leu Glu Ile Pro Asn																				
255 260 265 270																				
cta gcc aaa ctc tat aac att acc aac cac ccc tta aaa ggg agc ttg	925																			
Leu Ala Lys Leu Tyr Asn Ile Thr Asn His Pro Leu Lys Gly Ser Leu																				
275 280 285																				
act tta aaa ggc gct ata gaa caa agc ccc aaa ctt tta aaa gtc agc	973																			
Thr Leu Lys Gly Ala Ile Glu Gln Ser Pro Lys Leu Leu Lys Val Ser																				
290 295 300																				
ggc cat tca aat tta cta gac ggc gcg ctg gat ttc acg ctt tta aat	1021																			
Gly His Ser Asn Leu Leu Asp Gly Ala Leu Asp Phe Thr Leu Leu Asn																				
305 310 315																				
aaa gat ttg aaa ggg cgt ttt tcc aat att tcc act tta aaa gct tta	1069																			
Lys Asp Leu Lys Gly Arg Phe Ser Asn Ile Ser Thr Leu Lys Ala Leu																				
320 325 330																				
gat tta ttc cat tac cct aag ttt ttc caa tcc gtt gca gac gct aat	1117																			
Asp Leu Phe His Tyr Pro Lys Phe Phe Gln Ser Val Ala Asp Ala Asn																				
335 340 345 350																				

ttg gat tat gat ctt atc gct aag caa ggc gta ttg aaa gcc cgc cta 1165
 Leu Asp Tyr Asp Leu Ile Ala Lys Gln Gly Val Leu Lys Ala Arg Leu
 355 360 365
 aaa aac gca aga ttc ctc aaa aat gca ttc agc gat ttt ctc tac tcc 1213
 Lys Asn Ala Arg Phe Leu Lys Asn Ala Phe Ser Asp Phe Leu Tyr Ser
 370 375 380
 att tct aaa ttt gat att aca aaa gaa att tat aac gat gcc aat ctg 1261
 Ile Ser Lys Phe Asp Ile Thr Lys Glu Ile Tyr Asn Asp Ala Asn Leu
 385 390 395
 gta agc caa atc aac cag caa cgc ctg ctc tct gat ctg agt tta aaa 1309
 Val Ser Gln Ile Asn Gln Arg Leu Leu Ser Asp Leu Ser Leu Lys
 400 405 410
 agc ccc aaa acc caa ttg aaa atc cat aac ggt ttg ttg gat tta aac 1357
 Ser Pro Lys Thr Gln Leu Lys Ile His Asn Gly Leu Leu Asp Leu Asn
 415 420 425 430
 acc aaa caa atg aac atg ctc atg gat gcg gaa att tta aaa ttc att 1405
 Thr Lys Gln Met Asn Met Leu Met Asp Ala Glu Ile Leu Lys Phe Ile
 435 440 445
 ttt aaa atg aaa ctt caa ggc aac atg cac cag cca aaa ttt tct ctc 1453
 Phe Lys Met Lys Leu Gln Gly Asn Met His Gln Pro Lys Phe Ser Leu
 450 455 460
 att tta aac gaa aaa gcc att cag caa aac ttg caa caa ggc ttg aaa 1501
 Ile Leu Asn Glu Lys Ala Ile Gln Gln Asn Leu Gln Gln Gly Leu Lys
 465 470 475
 gaa atc tta aaa aac gac acc ctt aaa aaa ggt tta gat cat ttg ctt 1549
 Glu Ile Leu Lys Asn Asp Thr Leu Lys Lys Gly Leu Asp His Leu Leu
 480 485 490
 aaa gat gat aag ctc aaa gaa aag ctt gaa aaa ggg ctt aag ggg ctt 1597
 Lys Asp Asp Lys Leu Lys Glu Lys Leu Glu Lys Gly Leu Lys Gly Leu
 495 500 505 510
 ttt taaaaatttt aaaggataga aatggcgcac atttttagtta gcggggcgac 1650
 Phe
 ttcagggttt gga 1663

<210> 92

<211> 511

<212> PRT

<213> *Helicobacter pylori*

<400> 92

Met Lys Lys Leu Leu Tyr Thr Ile Leu Ala Leu Leu Leu Ile Gly Leu
 1 5 10 15
 Leu Thr Ile Tyr Leu Ile Leu Phe Thr Glu Trp Gly Asn Lys Ile Ile
 20 25 30
 Ala Ser Tyr Ile Glu Lys Lys Ile Asn Pro Asn Glu His Tyr Leu Ser
 35 40 45

Val	Lys	Thr	Phe	Lys	Leu	Arg	Phe	Asn	Ser	Leu	Asp	Phe	Lys	Ala	Gln	50	55	60
Ala	Asn	Asp	Asp	Ser	Thr	Leu	Ile	Leu	Lys	Gly	Asp	Phe	Ser	Leu	Leu	65	70	75
Lys	Gln	Ser	Val	Asn	Leu	Asn	Tyr	His	Ile	Asp	Ile	Lys	Asp	Leu	Arg	85	90	95
Ser	Phe	Lys	Glu	Trp	Ile	Pro	Tyr	Pro	Leu	Arg	Gly	Ala	Val	Ile	Thr	100	105	110
Ser	Gly	Asn	Ile	Lys	Gly	His	Arg	Lys	Ala	Leu	Met	Ile	Gln	Gly	Val	115	120	125
Ser	Asn	Val	Ala	Gln	Ser	His	Thr	Ala	Tyr	Asn	Ala	Leu	Leu	Asp	Asp	130	135	140
Phe	Lys	Leu	Ser	Arg	Leu	Asn	Leu	Asn	Ala	Gln	Asp	Ala	Asn	Leu	Glu	145	150	155
Asp	Leu	Leu	Tyr	Leu	Ile	Asn	Arg	Pro	Ala	Tyr	Ala	Asn	Ala	Lys	Val	165	170	175
Ser	Leu	Gln	Ala	Asp	Phe	Asn	Ser	Leu	Lys	Pro	Leu	Glu	Gly	His	Leu	180	185	190
Ile	Leu	Thr	Ala	Asn	Asn	Ala	Leu	Ile	Asn	Asn	Ala	Leu	Ile	Asn	Gln	195	200	205
Ile	Phe	His	Leu	Asn	Leu	Lys	Asp	Thr	Leu	Val	Phe	Ser	Leu	Ser	His	210	215	220
Ser	Ser	Asp	Phe	Lys	Gly	Asn	Lys	Ala	Ile	Ser	Asp	Thr	Thr	Leu	Thr	225	230	235
Ser	Pro	Leu	Ala	Asn	Phe	Lys	Ala	Leu	Lys	Ser	Glu	Tyr	Leu	Phe	Ser	245	250	255
Ile	Leu	Lys	Leu	Asn	Ala	Pro	Tyr	Thr	Leu	Glu	Ile	Pro	Asn	Leu	Ala	260	265	270
Lys	Leu	Tyr	Asn	Ile	Thr	Asn	His	Pro	Leu	Lys	Gly	Ser	Leu	Thr	Leu	275	280	285
Lys	Gly	Ala	Ile	Glu	Gln	Ser	Pro	Lys	Leu	Leu	Lys	Val	Ser	Gly	His	290	295	300
Ser	Asn	Leu	Leu	Asp	Gly	Ala	Leu	Asp	Phe	Thr	Leu	Leu	Asn	Lys	Asp	305	310	315
Leu	Lys	Gly	Arg	Phe	Ser	Asn	Ile	Ser	Thr	Leu	Lys	Ala	Leu	Asp	Leu	325	330	335
Phe	His	Tyr	Pro	Lys	Phe	Phe	Gln	Ser	Val	Ala	Asp	Ala	Asn	Leu	Asp	340	345	350
Tyr	Asp	Leu	Ile	Ala	Lys	Gln	Gly	Val	Leu	Lys	Ala	Arg	Leu	Lys	Asn	355	360	365
Ala	Arg	Phe	Leu	Lys	Asn	Ala	Phe	Ser	Asp	Phe	Leu	Tyr	Ser	Ile	Ser	370	375	380
Lys	Phe	Asp	Ile	Thr	Lys	Glu	Ile	Tyr	Asn	Asp	Ala	Asn	Leu	Val	Ser	385	390	395
Gln	Ile	Asn	Gln	Gln	Arg	Leu	Leu	Ser	Asp	Leu	Ser	Leu	Lys	Ser	Pro	405	410	415
Lys	Thr	Gln	Leu	Lys	Ile	His	Asn	Gly	Leu	Leu	Asp	Leu	Asn	Thr	Lys	420	425	430
Gln	Met	Asn	Met	Leu	Met	Asp	Ala	Glu	Ile	Leu	Lys	Phe	Ile	Phe	Lys	435	440	445
Met	Lys	Leu	Gln	Gly	Asn	Met	His	Gln	Pro	Lys	Phe	Ser	Leu	Ile	Leu	450	455	460
Asn	Glu	Lys	Ala	Ile	Gln	Gln	Asn	Leu	Gln	Gln	Gly	Leu	Lys	Glu	Ile	465	470	475
Leu	Lys	Asn	Asp	Thr	Leu	Lys	Lys	Gly	Leu	Asp	His	Leu	Leu	Lys	Asp	485	490	495
Asp	Lys	Leu	Lys	Glu	Lys	Leu	Glu	Lys	Gly	Leu	Lys	Gly	Leu	Phe		500	505	510

<210> 93
 <211> 947
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (292)...(645)

<400> 93
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 agaatggcaa aagcgcgaaa atgaagacag actctctgat tttgacgcta ttgcttcaaa 120
 ccatgcctct atcacgcctt taaatttaga cttaaccagt tatgatgatt tgaaaagtgt 180
 ggaatccttg catgagggaa tgttaaagtg agtaaaaagc accgcttggc ttttttaggg 240
 ctaattgttg gggttctatt cttctttagt gcgtgtgagc accgcctgca c atg ggg 297
 Met Gly
 1

tat tat tca gaa gtt aca ggg gat tat ttg ttc aat tat aat tcc act 345
 Tyr Tyr Ser Glu Val Thr Gly Asp Tyr Leu Phe Asn Tyr Asn Ser Thr
 5 10 15

atc gtg gtg gct tat gac aga agc gat gcg atg act tct tat tat atc 393
 Ile Val Val Ala Tyr Asp Arg Ser Asp Ala Met Thr Ser Tyr Tyr Ile
 20 25 30

aat gtg att gtt tat gaa ttg caa aaa tta ggc ttt tac aat gtc ttc 441
 Asn Val Ile Val Tyr Glu Leu Gln Lys Leu Gly Phe Tyr Asn Val Phe
 35 40 45 50

acg caa gcg gaa ttc cca cta gat aaa gcc aaa aat gtg atc tat gcg 489
 Thr Gln Ala Glu Phe Pro Leu Asp Lys Ala Lys Asn Val Ile Tyr Ala
 55 60 65

cgc att gtc cgt aac atc tca gct gtg ccg ttc tac caa tac aat tac 537
 Arg Ile Val Arg Asn Ile Ser Ala Val Pro Phe Tyr Gln Tyr Asn Tyr
 70 75 80

caa ctg att gat caa gtc aat aag cct tgt tat ttt ctt ggg ggg cag 585
 Gln Leu Ile Asp Gln Val Asn Lys Pro Cys Tyr Phe Leu Gly Gly Gln
 85 90 95

ttt tat tgc tct caa acc cta cgg att att acg cta tca atg gct tta 633
 Phe Tyr Cys Ser Gln Thr Leu Arg Ile Ile Thr Leu Ser Met Ala Leu
 100 105 110

gcg agc aaa ttt taatgagtgc taattcgcat tttatttttag attggtatga 685
 Ala Ser Lys Phe
 115

tgtggtgttg caaaaacggg ttttatatgt ggatgggagc gtgagcggga ggacttgcg 745
 ctatcagatg ctgtataggg atttgattaa aagcacgac aaacgcattg attttaaccg 805
 ccctgaacgc tactactaca atttaagact gccctttat cagccatgtt ataggcaatg 865
 aaatgggtat caggcgattg tatcaatttt gcgctagcca tgtggtgcgc aattgctctt 925
 ctttaaaatg cgctcaaaat at 947

<210> 94

<211> 118
 <212> PRT
 <213> Helicobacter pylori

<400> 94

Met	Gly	Tyr	Tyr	Ser	Glu	Val	Thr	Gly	Asp	Tyr	Leu	Phe	Asn	Tyr	Asn
1				5					10					15	
Ser	Thr	Ile	Val	Val	Ala	Tyr	Asp	Arg	Ser	Asp	Ala	Met	Thr	Ser	Tyr
		20						25					30		
Tyr	Ile	Asn	Val	Ile	Val	Tyr	Glu	Leu	Gln	Lys	Leu	Gly	Phe	Tyr	Asn
		35					40					45			
Val	Phe	Thr	Gln	Ala	Glu	Phe	Pro	Leu	Asp	Lys	Ala	Lys	Asn	Val	Ile
	50				55						60				
Tyr	Ala	Arg	Ile	Val	Arg	Asn	Ile	Ser	Ala	Val	Pro	Phe	Tyr	Gln	Tyr
65				70					75					80	
Asn	Tyr	Gln	Leu	Ile	Asp	Gln	Val	Asn	Lys	Pro	Cys	Tyr	Phe	Leu	Gly
			85					90						95	
Gly	Gln	Phe	Tyr	Cys	Ser	Gln	Thr	Leu	Arg	Ile	Ile	Thr	Leu	Ser	Met
			100					105					110		
Ala	Leu	Ala	Ser	Lys	Phe										
			115												

<210> 95
 <211> 875
 <212> DNA
 <213> Helicobacter pylori

<220>

<221> CDS

<222> (348)...(716)

<400> 95

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ttttgaaaat	tttaatcctt	ttttttatct	gtttaaacgc	attgttcgcc	ctagattcaa	120
acgcacttaa	agcagagatt	aaagaagttt	accttaaaga	atacaaagac	ttaaaattag	180
aaattgaaac	cattaactta	gaaatcccag	agcgcttttc	taacgcttcc	attttaagct	240
atgaattaaa	cgcttccaat	aagcttaaaa	aagatggggg	cgtgttttta	aggttggaaa	300
atgatcctaa	tttacgccta	ccggtgcgtt	atagcgtgat	aggcagc	atg cag gct	356
					Met Gln Ala	
					1	
ttt aaa agc gtt agc gcg att aaa aaa gat gaa aac atc acc gct aat	404					
Phe Lys Ser Val Ser Ala Ile Lys Lys Asp Glu Asn Ile Thr Ala Asn						
5 10 15						
aac act caa aaa gag cgc att ttg ttt ggt gcg ctt tct aac ccc tta	452					
Asn Thr Gln Lys Glu Arg Ile Leu Phe Gly Ala Leu Ser Asn Pro Leu						
20 25 30 35						
tta gag ggc gcg att gat aaa gtg agc gcg aaa aat ttt atc ccc cct	500					
Leu Glu Gly Ala Ile Asp Lys Val Ser Ala Lys Asn Phe Ile Pro Pro						
40 45 50						
aac acg ctt tta agc acg gat aaa acc caa gct tta att atc gtg cgt	548					
Asn Thr Leu Leu Ser Thr Asp Lys Thr Gln Ala Leu Ile Ile Val Arg						
55 60 65						

	1	5	
gaa gcc caa gaa atc gct aaa aaa gcc gtt aaa atc gtg ttt ttt tta			222
Glu Ala Gln Glu Ile Ala Lys Lys Ala Val Lys Ile Val Phe Phe Leu			
	10	15	20
ggg ctt gtg gtg gtg ctt ttg atg atg ata aac ctt tac atg ctc atc			270
Gly Leu Val Val Val Leu Leu Met Met Ile Asn Leu Tyr Met Leu Ile			
	25	30	35
aat caa atc aac gcg agc gct caa atg agc cac caa atc aaa aag ata			318
Asn Gln Ile Asn Ala Ser Ala Gln Met Ser His Gln Ile Lys Lys Ile			
	40	45	50
gaa gaa agg ctt aat cag gag caa aaa taaaaaaggc tttttggtat			365
Glu Glu Arg Leu Asn Gln Glu Gln Lys			
	55	60	
ttttacgatac aaatagtaaa gagcttatac			394

<210> 98
 <211> 62
 <212> PRT
 <213> Helicobacter pylori

<400> 98
Met Gln Lys Glu Gln Glu Ala Gln Glu Ile Ala Lys Lys Ala Val Lys
1 5 10 15
Ile Val Phe Phe Leu Gly Leu Val Val Val Leu Leu Met Met Ile Asn
20 25 30
Leu Tyr Met Leu Ile Asn Gln Ile Asn Ala Ser Ala Gln Met Ser His
35 40 45
Gln Ile Lys Lys Ile Glu Glu Arg Leu Asn Gln Glu Gln Lys
50 55 60

<210> 99
 <211> 516
 <212> DNA
 <213> Helicobacter pylori

<400> 99	
gtttgattta gttcaagagc ttttagaaga atttttgcaa agcggggcta aagagatttt	60
agaaaaggcg cagttgtttt aatgcgtttg tttatcgcg tagttttgtt ttggtggtgg	120
ttaagcttga acgctaaaga agcggatttt atctctgatt tagaatacgg gatggctctt	180
tataaaaacc ctaggggtgt tgcgtgcgcg aaatgccatg gcattaaagg cgaacaacaa	240
gaaatcacct tttattatga aaaaggcgag aaaaaaatcc tctacgcccc taaaatcaac	300
catttggtt ttaaaacctt taaagacgcc ttgagtttag gcaaaggcat gatgcctaaa	360
tacaatctca atttagaaga aatccaagcg atttatcttt atatcatctc ttttagagcat	420
aaagaagagc gtaaggattc tcctaagcct taatcaaagc gcttgattta tgctaaaatg	480
gagcgttgca tttttgtttt gattaaagaa ggggttc	516

<210> 100
 <211> 709
 <212> DNA
 <213> Helicobacter pylori

<400> 100

taagggatat	tgctaacgat	taagctgtat	tggaagagtt	tatdddgtcaa	gaattaatct	60
tgccdtgtgt	gattagtaac	acaaggcaag	tgtgataaac	cctactacaa	tttcaattca	120
aggagcctaa	ctaaaataaa	atgaacaatt	tcagttaggg	ctttattata	gcaaaaatta	180
tctaagatta	caaagggtag	cgtttctgtt	tttggattta	gagcgttatt	ttgattgttt	240
tgagtttaat	ttactttttg	tttaataata	aatccttaact	atcataaatg	tacaattaaa	300
gtattttaaa	aaatttttaa	acaaaaggat	ataaaatgaa	aaccattaga	aatagcgtgt	360
ttattggagc	gtctttactc	ggcggttgcg	ctagcgttga	ggcttatttt	gacgctttgc	420
atgttgctcg	cgttaaagac	gcttgtttat	agaaaaagaa	gcacaccaca	cgcccaaaga	480
ctttgatagc	ccttaccaca	ctgactaaac	cggcactagg	ttttagttgg	gggttttttag	540
gggtgttatt	ttagatactc	tctgttccct	taaagaaaat	aaatttctac	cataaaataa	600
aatcttaaat	taaggcgact	aaaaccccac	ttttaaaaaa	ttaaaaagcg	ttaagtaaga	660
cttatccaaa	aagcaaagaa	aatcaatttt	tccaaccact	ttttttaag		709

<210> 101
 <211> 33
 <212> DNA
 <213> Helicobacter pylori

<400> 101	
cgcgatccg	aaatagggtt gtttttaatt ttc
	33

<210> 102
 <211> 30
 <212> DNA
 <213> Helicobacter pylori

<400> 102	
ccgctcgagt	taaaaaaga gtttgataa
	30

<210> 103
 <211> 25
 <212> DNA
 <213> Helicobacter pylori

<400> 103	
ggggatcctt	ggtagaattg aatca
	25

<210> 104
 <211> 23
 <212> DNA
 <213> Helicobacter pylori

<400> 104	
ggaattccta	aaacaagaac gcg
	23

<210> 105
 <211> 25
 <212> DNA
 <213> Helicobacter pylori

<400> 105	
ggggatcctt	ttttcaaaaa caata
	25

<210> 106
 <211> 23
 <212> DNA
 <213> Helicobacter pylori

<400> 106 ggaattctca cattgttttg ctc	23
<210> 107 <211> 23 <212> DNA <213> Helicobacter pylori	
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<210> 108 <211> 25 <212> DNA <213> Helicobacter pylori	
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<210> 109 <211> 32 <212> DNA <213> Helicobacter pylori	
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<210> 111 <211> 24 <212> DNA <213> Helicobacter pylori	
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<210> 112 <211> 24 <212> DNA <213> Helicobacter pylori	
<400> 112 ccgctcgagt taaaatttgc tcgc	24